



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102152

**TO: John Ulm
Location: CM-1/10D19
Art Unit: 1646
Wednesday, August 27, 2003
Case Serial Number: 09988745**

**From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954**

paul.schulwitz@uspto.gov

Search Notes

Examiner Ulm,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954

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SEARCH REQUEST FORM

Access DB# 102152

OL 8/26

RECEIVED Scientific and Technical Information Center

Requester's Full Name: AUG 22 1988 41m Examiner #: 69507 Date: 8-22-87
 Art Unit: 1646 Phone Number: 308-4008 Serial Number: 09/988745
 Mail Box and Bldg/Room Location: CM1 Results Format Preferred (circle): PAPER DISK E-MAIL
10217

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

please send SEQ ID NO: 2 of
 09/988,745.
 reg 2 - 337 AN

STAFF USE ONLY

Type of Search		Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/26</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/27</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:23:02 ; Search time 25 seconds
(without alignments)
1778.844 M.Illion cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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18: /cgn2_6/ptodata/1/pubppa/US60_PUB.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1785	100.0	337	US-10-180-946-2	Sequence 2, Appl1
2	1785	100.0	337	US-10-225-567A-358	Sequence 358, App
3	1703	95.4	321	US-10-330-220-4	Sequence 4, Appl1
4	1703	95.4	321	US-10-251-852-5	Sequence 5, Appl1
5	812.5	45.5	348	US-10-225-567A-645	Sequence 645, App
6	786.5	44.1	345	US-09-995-225-10	Sequence 10, Appl
7	786.5	44.1	345	US-09-782-974C-84	Sequence 84, Appl
8	786.5	44.1	345	US-09-995-225-10	Sequence 10, Appl
9	786.5	44.1	345	US-10-225-567A-685	Sequence 685, App
10	786.5	44.1	345	US-10-251-852-2	Sequence 2, Appl1
11	785.5	44.0	342	US-09-995-225-14	Sequence 14, Appl
12	785.5	44.0	342	US-09-791-932-118	Sequence 118, Appl
13	785.5	44.0	342	US-09-995-225-14	Sequence 14, Appl
14	785.5	44.0	342	US-10-225-567A-687	Sequence 687, App
15	783.5	43.9	342	US-10-330-220-2	Sequence 2, Appl1

16	735.5	41.2	351	US-09-474-696-2	Sequence 2, Appl1
17	735.5	41.2	351	US-10-307-736-2	Sequence 2, Appl1
18	696.5	39.0	306	US-10-225-567A-577	Sequence 577, App
19	677.5	38.0	339	US-09-995-225-12	Sequence 12, Appl
20	677.5	38.0	339	US-09-782-974C-90	Sequence 90, Appl
21	677.5	38.0	339	US-09-995-225-12	Sequence 12, Appl
22	677.5	38.0	339	US-10-267-217-6	Sequence 6, Appl1
23	677.5	38.0	339	US-10-225-567A-639	Sequence 639, App
24	674.5	37.8	343	US-09-742-869-2	Sequence 2, Appl1
25	674.5	37.8	343	US-10-225-567A-579	Sequence 579, App
26	673.5	37.7	296	US-10-251-852-6	Sequence 6, Appl1
27	617.5	34.6	332	US-10-267-217-4	Sequence 8, Appl1
28	543.5	30.4	296	US-09-782-974C-88	Sequence 88, Appl1
29	540.5	30.3	241	US-09-782-974C-46	Sequence 46, Appl
30	455.5	25.5	388	US-09-989-861-8	Sequence 8, Appl1
31	455.5	25.5	388	US-10-157-031-123	Sequence 123, App
32	455.5	25.5	388	US-10-157-031-124	Sequence 124, App
33	455.5	25.5	388	US-10-225-567A-18	Sequence 18, Appl
34	446.5	25.0	387	US-09-989-861-2	Sequence 2, Appl1
35	446.5	25.0	406	US-09-989-861-4	Sequence 4, Appl1
36	435.5	24.4	508	US-10-270-333-69	Sequence 69, Appl
37	432.5	24.2	466	US-09-992-238-19	Sequence 19, Appl
38	432.5	24.2	466	US-09-992-238-22	Sequence 22, Appl
39	431	24.1	241	US-10-017-161-1182	Sequence 1182, Ap
40	419	23.5	497	US-10-052-589-2	Sequence 2, Appl1
41	419	23.5	515	US-10-238-129-9	Sequence 9, Appl1
42	419	23.5	515	US-10-238-129-10	Sequence 10, Appl
43	419	23.5	515	US-10-238-667-9	Sequence 9, Appl1
44	419	23.5	515	US-10-238-667-10	Sequence 10, Appl
45	418	23.4	517	US-09-951-622-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-180-946-2
; Sequence 2, Application US/10180946
; Publication No. US2003093825A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: PUTATIVE NEUROTRANSMITTER RECEPTOR (P2NR)
; FILE REFERENCE: R-336
; TITLE OF INVENTION: DISRUPTIONS, COMPOSITIONS AND METHODS RELATING THERETO
; CURRENT APPLICATION NUMBER: US/10/180,946
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/301,060
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/340,380
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-180-946-2

Query Match 100.0%; Score 1785; DB 15; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-153;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRAVFIGAEHHPAFCYGVNSCPRTVHTLGIOVYITLCAGMIIYGVAFVAFVS 60
OY YFRAHTPTNELLSSALADMFGLVLPSTIRSVESCFSGDFLCRLHTTYLDTEFCUL 120
Db YFRAHTPTNELLSSALADMFGLVLPSTIRSVESCFSGDFLCRLHTTYLDTEFCUL 120
OY 61 YFRAHTPTNELLSSALADMFGLVLPSTIRSVESCFSGDFLCRLHTTYLDTEFCUL 120
Db 61 YFRAHTPTNELLSSALADMFGLVLPSTIRSVESCFSGDFLCRLHTTYLDTEFCUL 120
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DB 181 QMLEEMPCVSGCOLLNKFMGMNPLFEVPCILMISLYKIFVATROAOQITLTSKSL 240
QY 241 AGAAKHERKAKKTIGIYVGYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNAC 300
DB 241 AGAAKHERKAKKTIGIYVGYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNAC 300
QY 301 NPITVSYQWFRKALKLTLSQKVFSPQTRTVDLXOE 337
DB 301 NPITVSYQWFRKALKLTLSQKVFSPQTRTVDLXOE 337

RESULT 2
US-10-225-567A-358
; Sequence 358, Application US/10225567A
; Publication No. US20030113796A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 358
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-358

Query Match 100.0%; Score 1785; DB 15; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-153;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MRAVFIGAEERHPAFCYQVNGSCPRVHTLGIQVLYITLCAAGMLITVGNVFAVAVS 60
QY 61 YFKALHPTNPLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCT 120
DB 61 YFKALHPTNPLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCT 120
QY 121 SIFHLCTSIDRHCAICDPLLYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERRLS 180
DB 121 SIFHLCTSIDRHCAICDPLLYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERRLS 180
QY 181 QMLEEMPCVSGCOLLNKFMGMNPLFEVPCILMISLYKIFVATROAOQITLTSKSL 240
DB 181 QMLEEMPCVSGCOLLNKFMGMNPLFEVPCILMISLYKIFVATROAOQITLTSKSL 240
QY 241 AGAAKHERKAKKTIGIYVGYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNAC 300
DB 241 AGAAKHERKAKKTIGIYVGYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNAC 300
QY 301 NPITVSYQWFRKALKLTLSQKVFSPQTRTVDLXOE 337
DB 301 NPITVSYQWFRKALKLTLSQKVFSPQTRTVDLXOE 337

RESULT 3
US-10-330-220-4
; Sequence 4, Application US/10330220
; Publication No. US20030113789A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00755CON
; CURRENT APPLICATION NUMBER: US/10/330,220
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/637,603
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/192,326
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-330-220-4

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Best Local Similarity 100.0%; Pred. No. 4e-146;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 CYQVNGSCPRVHTLGIQVLYITLCAAGMLITVGNVFAVAVSFRALHTPTNPLLSL 76
DB 1 CYQVNGSCPRVHTLGIQVLYITLCAAGMLITVGNVFAVAVSFRALHTPTNPLLSL 76
QY 77 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCTSIDRHCAI 136
DB 77 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCTSIDRHCAI 120
QY 61 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCTSIDRHCAI 120
DB 61 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLTFLCCTSIDRHCAI 120
QY 137 CDPLLYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERRLSQMLEEMPCVSGCOLL 196
DB 121 CDPLLYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERRLSQMLEEMPCVSGCOLL 180
QY 197 NKEFGWLNPLFEVPCILMISLYKIFVATROAOQITLTSKSLAGAAKHERKAKKTIGI 256
DB 181 NKEFGWLNPLFEVPCILMISLYKIFVATROAOQITLTSKSLAGAAKHERKAKKTIGI 240
QY 257 VVGIIYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNACNPITVSYQWFRKAL 316
DB 241 VVGIIYLLCWLPTTIDTMDSLHFTTTPPLVDFITWFAVFNACNPITVSYQWFRKAL 300
QY 317 KLTLSQKVFSPQTRTVDLXOE 337
DB 301 KLTLSQKVFSPQTRTVDLXOE 321

RESULT 4
US-10-251-852-5
; Sequence 5, Application US/10251852
; Publication No. US20030119144A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CLO00899-CON
; CURRENT APPLICATION NUMBER: US/10/251,852
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 09/781,559
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/694,821
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/208,929
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Human
US-10-251-852-5
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Best Local Similarity 100.0%; Pred. No. 4e-146;
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Qy	77	ALADMFGLIYVLP.LSTIRSEVSCWFGDFLCRLHYLDYI.FCLTSIFHLCTISDRHCAL	136
Db	61	ALADMFGLIYVLP.LSTIRSEVSCWFGDFLCRLHYLDYI.FCLTSIFHLCTISDRHCAL	120
Qy	137	CDBLLYPSKFTYVVALRYILIAAGVPAAYTSLELYTDVYI.TRLSQWLEMPQVSCOLL	186
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Qy	197	NKFWGMLNPPLFVNPCLIMISLYVKI.FVAVATQAQOITTYI.SKSLAGAAKHERKAKTLGI	256
Db	181	NKFWGMLNPPLFVNPCLIMISLYVKI.FVAVATQAQOITTYI.SKSLAGAAKHERKAKTLGI	240
Qy	257	VWGIIYLLCWL.PFIIDNMDSLHFTTPPLVNDIF.FWFAVY.NSACNPITYVSQWFKRAL	316
Db	241	VWGIIYLLCWL.PFIIDNMDSLHFTTPPLVNDIF.FWFAVY.NSACNPITYVSQWFKRAL	300
Qy	317	KLTIISOKEVSPQRTVDLXOE	337
Db	301	KLTIISOKEVSPQRTVDLXOE	321

RESULT 5

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US-10-225-567A-645
: Sequence 645: Application US/10225567A
: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenna C.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTISENSE PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
: FILE REFERENCE: 1990-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 645
: LENGTH: 348
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-225-567A-645

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Query Match	45.5%;	Score 812.5;	DB 15;	Length 348;
Best Local Similarity	46.1%;	Pred. No. 1.4e-65;		
Matches 152;	Conservative 64;	Mismatches 105;	Indels 9;	Gaps 3;

[illegible]

Dd 254 RKAAKTLGTMAAEFLYSWLPYLVDVIDAYANMETTPPIYVEITLWCYTINSAMNPLIYA F 313

Q7 308 SYOWFRKALKLTLSQVWFSPQTIRVDLYOE 337
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Dd 314 FYQMFGKATLIYSGKVLRFTDSSTNTNLPS E 343

RESULT 6

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US-09-995-225-10  
Sequence ID: Application US/09995225  
Publication No.: US20020193584A1  
  
GENERAL INFORMATION:  
APPLICANT: Chen, Kuoping  
APPLICANT: Chu, Zhi Liang  
APPLICANT: Dang, Huong T.  
APPLICANT: Lowitz, Kevin P.  
APPICANT: Pride, Cameron  
  
TITLE OF INVENTION: Receptors And No. US70020193584A1-Endogenous Versions Of Huma  
TITLE OR INVENTION: Receptors  
FILE REFERENCE: ARKN-0308  
  
CURRENT APPLICATION NUMBER: US/09/995,225  
CURRENT FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: PCT/US99/23938  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/253,404  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/255,366  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/270,286  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/282,365  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/270,266  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/282,032  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/282,358  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/282,356  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/290,917  
PRIOR FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: 60/309,208  
PRIOR FILING DATE: 2001-07-31  
NUMBER OF SEQ ID NOS: 67  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 345  
TYPE: PRY  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: No. US20020193584A1 Sequence  
US-09-995-225-10
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Best Local Similarity	44.28	Pred. No. 3e-63		
Matches 146; Conservative	70	Mismatches 105	Indels 9	Gaps 3

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Db 14 CYANVGSGCKIPFSGSGSVILYIVFGFCVAVLAVGNMLVMSILHFKQLHSPNPLVAV 73
QY 76 LALADMFGLVLPLESTIRSVESCFPGDFLCRLHTYVLDTFCLTSIPHLCFISIDRCA 135
Db 74 LAACDELGVYVAFPEEMARVIESCMTFGMSFTFTCCDVAFCTSSLEHLCTISIDRIA 133
QY 136 ICDPLLPKFTVAVRLRYILLAGWCVAAVTSILFTYDVVETRLISOMLEEMPCVGSQQL 195
Db 134 VEDPILVYPRFTYSVSGICISVSMILPLMTSAAVYFTGVYDGLLESDALNCTGGCQYV 193
QY 196 LNFWMGLNPLEFVPCLMISLVYKIEVAVATRAQOI-TTLTSS-----LAGAAKHE 247

Db 194 VNQMWVLTDFLSFPIPFIMILLGNIFLVARQAKIENTGSKTESSESRYKARVARE 253
QY 248 RKAAKTIGVYVGLICWLPETIDMWSLHFTPLVDFIEMFAVENSACNPITVE 307
Db 254 RKAATIGVYVAVMISMILPISIDSLDAFMGFTTPACIYETICMCATYNSANMPLIYAL 313
QY 308 SYQMFRAKALITLSQKVFSPQTRVDLYQX 337
Db 314 FYPMFRRAIKIVYTGVOVLKNSATMNLFE 343

RESULT 7

US-09-782-974C-84
; Sequence 84, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHR311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/774,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-84

Query Match 44.1% Score 786.5; DB 11; Length 345;
Best Local Similarity 44.2% Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY 17 CY-OVNCSCPRTVVTGIGQIVLYLTCAAGMLIIVLGNVFAVAFYKALHTPTNELLIS 75
Db 14 CYANVNSCVKIPSPGSRVILYVFGAVLANVFGMLVWISLHFKQLHSPNELLVAS 73
QY 76 LALADMFGLIYVPLSTIRSVESCFMGDFLCRLHTYLDLFCULTSIFHLCFISIDRHCA 135
Db 74 LACADFLVGVYVMPFSWVRVESCVMYGRSFCFPHCCDVAFCYSSLFHLCFISIDRYIA 133
QY 136 ICDPLPSKFTVVALRYTLAGWGPAAVTSFLTYDVTETRLSQMLEEPCVGSQOL 195
Db 134 VTDPVLVPIKFTVSVSGICISVSWILPLMTSGAVFYGVDDGLLELSDALMCTGGCQTV 193
QY 196 LNKFMGLNPFLEFVPLIMISLVYKIFVAVTRQAOOI-TTLLSKS-----LAGAAKHE 247
Db 194 VNQMWVLTDFLSFPIPFIMILLGNIFLVARQAKIENTGSKTESSESRYKARVARE 253

QY 248 RKAATIGVYVGLICWLPETIDMWSLHFTPLVDFIEMFAVENSACNPITVE 307
Db 254 RKAATIGVYVAVMISMILPISIDSLDAFMGFTTPACIYETICMCATYNSANMPLIYAL 313
QY 308 SYQMFRAKALITLSQKVFSPQTRVDLYQX 337
Db 314 FYPMFRRAIKIVYTGVOVLKNSATMNLFE 343

RESULT 8

US-09-995-225-10
; Sequence 10, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Endogenous And No. US20030139588A9- Endogenous Versions of Huma
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-10

Query Match 44.1% Score 786.5; DB 12; Length 345;
Best Local Similarity 44.2% Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY 17 CY-OVNCSCPRTVVTGIGQIVLYLTCAAGMLIIVLGNVFAVAFYKALHTPTNELLIS 75
Db 14 CYANVNSCVKIPSPGSRVILYVFGAVLANVFGMLVWISLHFKQLHSPNELLVAS 73
QY 76 LALADMFGLIYVPLSTIRSVESCFMGDFLCRLHTYLDLFCULTSIFHLCFISIDRHCA 135
Db 74 LACADFLVGVYVMPFSWVRVESCVMYGRSFCFPHCCDVAFCYSSLFHLCFISIDRYIA 133
QY 136 ICDPLPSKFTVVALRYTLAGWGPAAVTSFLTYDVTETRLSQMLEEPCVGSQOL 195

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Db      134 VDPDLYPTKFTVSVSGICISVMIPLMTSGAVYTGVIDGLEELSDALNCIGCCQY 193
QY      196 LNFKMGWLNPLEFVPCILMISLYKIFVATROAOOI-TTLSKS-----LAGAKHE 247
       194 VNQNMVLTDFLSFIFTFIMILYKGNIFLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCWLPEFTIDVDSLHFTTPPLV/DITFWAFNSACNPIIYVF 307
       254 RKAATLGIVVVAFMISMLPYSDSLDAMGFTTPACI/EICWCAYNSANMPLIYAL 313
QY      308 SYOMFRKALKLTLSOKVFSPTQRTVDLYOE 337
       314 FYPMFRKAIKIVITGVQLKNSSATMNLFSE 343
Db

RESULT 9
US-10-225-567A-685
; Sequence 685, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 685
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-225-567A-685

Query Match      44.1%; Score 786.5; DB 15; Length 345;
Best Local Similarity 44.2%; Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY      17 CY-QVNGSCPRTVHTIGIQLVITLCAAGMLIYLVGNV/AFAVSFKALHTPTNELL 75
       14 CYANVNGSCVKIPFSPGSRVILYIVGFGAVLAVFGML/MISILHKQLHSPTNFLVAS 73
QY      76 LADADFEGLLVPLSTIRVESQWFRGDFLCRLHTYLDLFLCLTSTFHLCTISIDRCA 135
       74 LACADFLVGVTVMPFSVNRVESCWFGRSFCFTHCCD/AFCYSSLFHLCTISIDRYIA 133
Db
QY      136 ICDPLTPSKFTVVALRYILAGWVPAATYSLFLYVDV/ETRLSQWLEEMPCVGSQCL 195
       134 VTPDLYPTKFTVSVSGICISVMIPLMTSGAVYTGVIDGLEELSDALNCIGCCQY 193
QY      196 LNFKMGWLNPLEFVPCILMISLYKIFVATROAOOI-TTLSKS-----LAGAKHE 247
       194 VNQNMVLTDFLSFIFTFIMILYKGNIFLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCWLPEFTIDVDSLHFTTPPLV/DITFWAFNSACNPIIYVF 307
       254 RKAATLGIVVVAFMISMLPYSDSLDAMGFTTPACI/EICWCAYNSANMPLIYAL 313
Db
QY      308 SYOMFRKALKLTLSOKVFSPTQRTVDLYOE 337
       314 FYPMFRKAIKIVITGVQLKNSSATMNLFSE 343
Db

RESULT 10
US-10-251-852-2
; Sequence 2, Application US/10251852
; Publication No. US20030119144A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
```

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; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000899-CON
; CURRENT APPLICATION NUMBER: US/10/251,852
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 09/781,559
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/694,821
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/208,929
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Human
US-10-251-852-2

Query Match      44.1%; Score 786.5; DB 15; Length 345;
Best Local Similarity 44.2%; Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY      17 CY-QVNGSCPRTVHTIGIQLVITLCAAGMLIYLVGNV/AFAVSFKALHTPTNELL 75
       14 CYANVNGSCVKIPFSPGSRVILYIVGFGAVLAVFGML/MISILHKQLHSPTNFLVAS 73
QY      76 LADADFEGLLVPLSTIRVESQWFRGDFLCRLHTYLDLFLCLTSTFHLCTISIDRCA 135
       74 LACADFLVGVTVMPFSVNRVESCWFGRSFCFTHCCD/AFCYSSLFHLCTISIDRYIA 133
Db
QY      136 ICDPLTPSKFTVVALRYILAGWVPAATYSLFLYVDV/ETRLSQWLEEMPCVGSQCL 195
       134 VTPDLYPTKFTVSVSGICISVMIPLMTSGAVYTGVIDGLEELSDALNCIGCCQY 193
QY      196 LNFKMGWLNPLEFVPCILMISLYKIFVATROAOOI-TTLSKS-----LAGAKHE 247
       194 VNQNMVLTDFLSFIFTFIMILYKGNIFLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCWLPEFTIDVDSLHFTTPPLV/DITFWAFNSACNPIIYVF 307
       254 RKAATLGIVVVAFMISMLPYSDSLDAMGFTTPACI/EICWCAYNSANMPLIYAL 313
QY      308 SYOMFRKALKLTLSOKVFSPTQRTVDLYOE 337
       314 FYPMFRKAIKIVITGVQLKNSSATMNLFSE 343
Db

RESULT 11
US-09-995-225-14
; Sequence 14, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Huma
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
```

```
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,365
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 342
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-14
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Query Match      44.0%; Score 785.5; DB 10; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;
```

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OY 17 CYQ-VNGSCPRTVTGIGIQLIYVLTCAAGMLIYGVNFVAVSYFKALHTPTNFIILS 75
   ||| ||||| | : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 13 CYEVNNGSCITPTSPSGSRVILYTAFFSGSLAVFGNLLVMTSVLHKQLHSPNFIILAS 72
OY 76 LALADMFGLLVLPSTIRSVESCMFEGDFLCRLHTYLDLTCFSLIFHLCFISIDRRCA 135
   ||| ||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 73 LACADFLGVVLMFMSVRVESCWFYGAKECTLHSCDDVAFCSYVHLGFCIDRYIV 132
OY 136 ICDPLLPKSTTVVALRYIILAGVCPAATYSLFLYDYVETRLSQMLEHPVCGSCQL 195
   : ||| : : ||| : : | : : | : : | : : | : : | : : | : : | : : |
DB 133 VTDLVATKFTVSVSIGCISVSWILPLTVSGAVFYGVNDGEEIVSALNCVGGCOII 192
OY 196 LNKFMGLNFPLEFVPCIMISLVKIFVATROAOITTLTKSLAG-----AKHE 247
   : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 193 VSQGWLIDFLFFIPLVMIILSKIFLAKQDAIKETTSVVESSSESKIRVAKRE 252
OY 248 RKAATIGIVVGIILCWLPEITDMVDSLHFTTPPLVDFITWFAVFNACNPITIVF 307
   ||||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 253 RKAATIGVVLAVISWLPYTVDLIDAFMGFLTPAYIVEICMSAVYNSAMNPLIYAL 312
OY 308 SYQWFRKAKITLSQKVFSPQTRVVDLXQE 337
   | ||||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 313 FYPMFRRAIKILISGDVLKASSSTISLE 342
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RESULT 12
US-09-791-932-118

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;; Sequence 118, Application US/09791932
;; Publication No. US20030003451A1
;; GENERAL INFORMATION:
;; APPLICANT: Vogeli, Gabriel
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Hiesbach, Ronald R.
;; APPLICANT: Lind, Peter
;; APPLICANT: Kayles, Paul S.
;; APPLICANT: Ruff, Valerie
;; APPLICANT: Huff, Rita M.
;; APPLICANT: Wood, Linda S.
;; TITLE OR INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
;; FILE REFERENCE: 00325.051
;; CURRENT APPLICATION NUMBER: US/09/791.932
;; PRIOR APPLICATION NUMBER: 60/184,305
;; PRIOR FILING DATE: 2000-02-23
```

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;; PRIOR APPLICATION NUMBER: 60/184,304
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,303
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,397
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,247
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/188,880
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: 60/217,369
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/217,370
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/218,492
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR APPLICATION NUMBER: 60/186,810
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/188,064
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: 60/186,457
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: 60/213,861
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: 60/194,344
;; PRIOR FILING DATE: 2000-04-03
;; PRIOR APPLICATION NUMBER: 60/218,337
;; PRIOR FILING DATE: 2000-07-14
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 118
;; LENGTH: 342
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-791-932-118
```

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Query Match      44.0%; Score 785.5; DB 11; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;
```

```
OY 17 CYQ-VNGSCPRTVTGIGIQLIYVLTCAAGMLIYGVNFVAVSYFKALHTPTNFIILS 75
   ||| ||||| | : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 13 CYEVNNGSCITPTSPSGSRVILYTAFFSGSLAVFGNLLVMTSVLHKQLHSPNFIILAS 72
OY 76 LALADMFGLLVLPSTIRSVESCMFEGDFLCRLHTYLDLTCFSLIFHLCFISIDRRCA 135
   ||| ||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 73 LACADFLGVVLMFMSVRVESCWFYGAKECTLHSCDDVAFCSYVHLGFCIDRYIV 132
OY 136 ICDPLLPKSTTVVALRYIILAGVCPAATYSLFLYDYVETRLSQMLEHPVCGSCQL 195
   : ||| : : ||| : : | : : | : : | : : | : : | : : | : : | : : |
DB 133 VTDLVATKFTVSVSIGCISVSWILPLTVSGAVFYGVNDGEEIVSALNCVGGCOII 192
OY 196 LNKFMGLNFPLEFVPCIMISLVKIFVATROAOITTLTKSLAG-----AKHE 247
   : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 193 VSQGWLIDFLFFIPLVMIILSKIFLAKQDAIKETTSVVESSSESKIRVAKRE 252
OY 248 RKAATIGIVVGIILCWLPEITDMVDSLHFTTPPLVDFITWFAVFNACNPITIVF 307
   ||||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 253 RKAATIGVVLAVISWLPYTVDLIDAFMGFLTPAYIVEICMSAVYNSAMNPLIYAL 312
OY 308 SYQWFRKAKITLSQKVFSPQTRVVDLXQE 337
   | ||||| : : : : : | : : : : | : : : : | : : : : | : : : : |
DB 313 FYPMFRRAIKILISGDVLKASSSTISLE 342
```

RESULT 13
US-09-995-225-14

```
;; Sequence 14, Application US/09995225
;; Publication No. US20030139588A9
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Ruoping
;; APPLICANT: Chu, Zhi Liang
;; APPLICANT: Dang, Huang T.
```

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; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139518A9-Endogenous Versions of Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 342
; TYPE: PRN
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: No. US2003013958A9el Sequence
US-09-995-225-14

Query Match      44.0%; Score 785.5; DB 12; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;

QY 17 CYQ-VNGSCPRVHTLGIOLVYITLCAAGMLIIVLGNVFAVAFVSKALHTPTNELLIS 75
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 CYEDVNGSCIEFTYSGSRVILYTAFFSGSLAVFGMLVMTSVLHKQHSPTNELLIS 72
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 LALADMFGLLVLPSTIRVESCWFPGDFLCRLHYLDTLFCLTSTIFHLCTSIDRHC 135
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 LACADFLVGTVMILFNVRTVESCWFYGAFCFTHSCDVAFCYSSVHLCTFICIDRYIV 132
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 136 ICDBLLYPSKFTYVALRYLILAGMVAATSLFELTDVYETLSQMLEMPVCGSCOLL 195
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 VTPDLVATKFTYVSGICISVSMILPLTYSGAVFTTGVDGLLEELVSALNCVGGCQII 192
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 196 LNFQWMLNPLFEVPCILMISLYKIFVATROAOITLTKSLAGA-----AKHE 247
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 VSGWGLIDPLFFIPFLVMIILYKIFLAKQAKIETTSKVSSESSYKIRAKRE 252
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 248 RKAATLGIYVGIYLLCMLPFTIDMVDLSLHFTTPPLVDFIETWAFNSACNPIIYVF 307
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 RKAATLGIYVLAFAVISMLPYTDILIDAFMGFLTPAYIYEICQMSAYNSANPLIYAL 312
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 SYQWFRKALKLTISQKVFSPQTRVDLYOE 337
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 FYWFRKALKLTISQVLAASSSTISLFL 342
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-225-567A-687
; Sequence 687, Application US/10225567A

```

```

; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 687
; LENGTH: 342
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-225-567A-687

Query Match      44.0%; Score 785.5; DB 15; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;

QY 17 CYQ-VNGSCPRVHTLGIOLVYITLCAAGMLIIVLGNVFAVAFVSKALHTPTNELLIS 75
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 CYEDVNGSCIEFTYSGSRVILYTAFFSGSLAVFGMLVMTSVLHKQHSPTNELLIS 72
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 LALADMFGLLVLPSTIRVESCWFPGDFLCRLHYLDTLFCLTSTIFHLCTSIDRHC 135
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 LACADFLVGTVMILFNVRTVESCWFYGAFCFTHSCDVAFCYSSVHLCTFICIDRYIV 132
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 136 ICDBLLYPSKFTYVALRYLILAGMVAATSLFELTDVYETLSQMLEMPVCGSCOLL 195
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 VTPDLVATKFTYVSGICISVSMILPLTYSGAVFTTGVDGLLEELVSALNCVGGCQII 192
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 196 LNFQWMLNPLFEVPCILMISLYKIFVATROAOITLTKSLAGA-----AKHE 247
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 VSGWGLIDPLFFIPFLVMIILYKIFLAKQAKIETTSKVSSESSYKIRAKRE 252
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 248 RKAATLGIYVGIYLLCMLPFTIDMVDLSLHFTTPPLVDFIETWAFNSACNPIIYVF 307
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 RKAATLGIYVLAFAVISMLPYTDILIDAFMGFLTPAYIYEICQMSAYNSANPLIYAL 312
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 SYQWFRKALKLTISQKVFSPQTRVDLYOE 337
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 FYWFRKALKLTISQVLAASSSTISLFL 342
   ||:||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-10-330-220-2
; Sequence 2, Application US/10330220
; Publication No. US20030113789A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000755CON
; CURRENT APPLICATION NUMBER: US/10/330,220
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/637,603
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/192,326
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRN
; ORGANISM: HOMO SAPIEN
US-10-330-220-2

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2003, 14:21:02 ; Search time 44 Seconds
(without alignments)
1215.701 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
Sequence: 1 MRAVFIGAEHHPAFCYGV.....LFLSQVFSPQRTVDLYOE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA1980.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	337	18	AAW09110
2	1785	100.0	337	20	AA13736
3	1785	100.0	337	23	ABR78232
4	1785	100.0	337	24	ABP56910
5	1785	100.0	337	24	ABR99760
6	1785	100.0	337	24	ABR81936
7	1703	95.4	331	22	AA65596
8	812.5	45.5	339	24	ABJ37891
9	812.5	45.5	348	21	AA18764

10	812.5	45.5	348	23	ABR98168	Human AXOR 106 aml
11	812.5	45.5	348	24	ABR81735	Human trace amine
12	795.5	44.6	338	21	AA18765	Amino acid sequenc
13	786.5	44.1	345	22	AA680970	Human nGPR40 #2.
14	786.5	44.1	345	23	ABR93788	Human G-protein-co
15	786.5	44.1	345	23	ABR52417	Human G-protein-co
16	786.5	44.1	345	23	ABU04072	Human G-protein co
17	786.5	44.1	345	23	AAU97600	Human G-protein co
18	786.5	44.1	345	24	ABP73007	Amino acid sequenc
19	786.5	44.0	342	22	ABR81756	Human trace amine
20	785.5	44.0	342	22	AAU25611	Human G-protein-co
21	785.5	44.0	342	22	ABU04074	Human G-protein co
22	785.5	44.0	342	23	AAO22086	Human G-protein co
23	785.5	44.0	342	24	ABP73040	Amino acid sequenc
24	785.5	44.0	342	24	ABR99740	Human trace amine
25	785.5	43.9	342	22	ABR81757	Human G-protein co
26	783.5	43.9	342	22	AA65595	Human trace amine
27	735.5	41.2	351	23	ABR79888	Human G-protein co
28	724.5	40.6	332	23	AAE23417	Human SNORF66 orph
29	697.5	39.1	306	18	AAW35831	Human G-protein co
30	697.5	39.1	306	24	ABR98746	Human G-protein co
31	696.5	39.0	295	22	AA672401	Human OR-1like poly
32	696.5	39.0	306	24	ABR57089	Human GPCR 58128 (
33	696.5	39.0	306	24	ABR81701	Human G-protein-co
34	686	38.4	319	22	AA672332	Human OR-1like poly
35	677.5	38.0	338	22	AA680973	Human G-protein co
36	677.5	38.0	339	22	AA680973	Human nGPR56 #3.
37	677.5	38.0	339	22	AA649232	Human SNORF33 rece
38	677.5	38.0	339	23	ABR93791	Human G-protein-co
39	677.5	38.0	339	23	ABU04073	Human G-protein co
40	677.5	38.0	339	24	ABR81732	Human trace amine
41	674.5	37.8	343	19	AAW59907	Human HNHC132 (G-P
42	674.5	37.8	343	23	ABR81702	Human G-protein-co
43	670.5	37.6	339	24	ABR80694	Human trace amine
44	657	36.8	332	22	AA649234	Mouse SNORF33 rece
45	626	35.1	332	23	ABR80695	Rat trace amine re

ALIGNMENTS

RESULT 1	AAW09110	standard; Protein; 337 AA.
ID	AAW09110:	
XX	AAW09110:	
AC	AAW09110:	
XX	05-APR-1997	(first entry)
DT	05-APR-1997	
XX	Human amine receptor.	
DE	Human amine receptor.	
XX		
XX	Amine receptor; 7-transmembrane receptor; neurotransmitter;	
KW	signal transduction; therapy; diagnosis; agonist; antagonist.	
OS	Homo sapiens.	
PN	MO639440-AL.	
XX	12-DEC-1996.	
XX	06-JUN-1995;	95WO-US07221.
XX	06-JUN-1995;	95WO-US07221.
XX	06-JUN-1995;	95WO-US07221.
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
XX	L1 Y, Ruben SM;	
PI		
XX		
DR	WPI: 1997-043075/04.	
XX	N-PDB: AAT51051.	
XX		
PT	DNA encoding human amine receptor - used to identify agonists and	
PT	antagonists, or amine neurotransmitters	

XX Claim 8; Fig 1A-1C; 68pp; English.
 PS
 CC A novel human mature 7-transmembrane receptor (AA09110) was
 CC putatively identified as an amine receptor (hAR) on the basis of
 CC sequence homology to the rat amine receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (AA751051) obcd. from a human
 CC genomic library. Recombinant mature hAR can be expressed in host
 CC (e.g. E. coli, COS, insect) cells and used to raise antibodies, to
 CC identify amine neurotransmitters transported by hAR, and to screen
 CC for agonist/antagonist cpds. useful for treating conditions related
 CC to hAR under-/over-expression.
 CC
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1785; DB 18; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.5e-186;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVLGNVFAFVAVS 60
 DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVLGNVFAFVAVS 60
 QY 61 YFKALHPTNPLLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYLDLTLFCLT 120
 DB 61 YFKALHPTNPLLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYLDLTLFCLT 120
 QY 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 DB 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 QY 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 DB 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 QY 181 QMLEMPGVSCQLLNKFMGMNPLFEVPCIMISLYKIFVAVTRQAQOITTLSSKL 240
 DB 181 QMLEMPGVSCQLLNKFMGMNPLFEVPCIMISLYKIFVAVTRQAQOITTLSSKL 240
 QY 241 AGAAKHEKAKKTIGIVGIYLCMLPTIDTMDSLHFTTPPLVDFITFMAFVNSAC 300
 DB 241 AGAAKHEKAKKTIGIVGIYLCMLPTIDTMDSLHFTTPPLVDFITFMAFVNSAC 300
 QY 301 NPIIYVSQWFRKALKLTLSQKVFSPQTRTVDLXQE 337
 DB 301 NPIIYVSQWFRKALKLTLSQKVFSPQTRTVDLXQE 337
 RESULT 2
 AAY13736
 ID AAY13736 standard; Protein: 337 AA.
 XX
 AC AAY13736;
 DT 13-SEP-1999 (first entry)
 XX
 DE Human amine receptor polypeptide.
 XX
 KW Human; amine receptor; recombinant.
 XX
 OS Homo sapiens.
 XX
 PN US5928890-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 06-JUN-1995; 95US-0467559.
 XX
 PR 06-JUN-1995; 95US-0467559.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI L1 Y;
 XX
 DR WPI; 1999-429497/36.
 DR N-PSDB; AAX81288.
 XX

PT Human amine receptor polynucleotides, vectors and host cells
 XX
 PS Claim 1; Fig 1; 22pp; English.
 XX
 CC This sequence represents a human amine receptor polypeptide. Host cells
 CC transformed with a vector comprising the amine receptor coding sequence
 CC are used for the recombinant production of the polypeptide. The
 CC polypeptides are useful for treating conditions related to under-
 CC expression and over-expression of the human amine receptor.
 CC
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1785; DB 20; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.5e-186;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVLGNVFAFVAVS 60
 DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVLGNVFAFVAVS 60
 QY 61 YFKALHPTNPLLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYLDLTLFCLT 120
 DB 61 YFKALHPTNPLLSLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYLDLTLFCLT 120
 QY 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 DB 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 QY 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 DB 121 SIFHLCEFSIDRHCAICDPLLYPSKFTVVALRYILAGMGPAAVTSLELYTDVETRLS 180
 QY 181 QMLEMPGVSCQLLNKFMGMNPLFEVPCIMISLYKIFVAVTRQAQOITTLSSKL 240
 DB 181 QMLEMPGVSCQLLNKFMGMNPLFEVPCIMISLYKIFVAVTRQAQOITTLSSKL 240
 QY 241 AGAAKHEKAKKTIGIVGIYLCMLPTIDTMDSLHFTTPPLVDFITFMAFVNSAC 300
 DB 241 AGAAKHEKAKKTIGIVGIYLCMLPTIDTMDSLHFTTPPLVDFITFMAFVNSAC 300
 QY 301 NPIIYVSQWFRKALKLTLSQKVFSPQTRTVDLXQE 337
 DB 301 NPIIYVSQWFRKALKLTLSQKVFSPQTRTVDLXQE 337
 RESULT 3
 ABB78232
 ID ABB78232 standard; Protein: 337 AA.
 XX
 AC ABB78232;
 DT 25-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a human amine receptor.
 XX
 KW Human; amine receptor; G-protein coupled receptor; receptor;
 KW dopamine D2 receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002086362-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 20-NOV-2001; 2001US-0988745.
 XX
 PR 06-JUN-1995; 95US-0467559.
 XX
 PR 19-MAY-1999; 99US-0314006.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI L1 Y, Ruben SM;
 XX
 DR WPI; 2002-635676/68.
 DR N-PSDB; ABQ78643.
 XX
 PT Novel human amine receptor polypeptide useful as research agents and

PT materials for discovery of treatments and diagnostics to human disease

PS Claim 8; Fig 1; 24pp; English.

CC The present sequence represents a human amine receptor. The polypeptide

CC is a G-protein coupled receptor. It was identified as an amine receptor

CC as a result of amino acid sequence homology to the rat amine receptor.

CC The protein also exhibits homology to a human dopamine D2 receptor.

CC The polynucleotide sequence is used as a source of probes and primers,

CC and for chromosome mapping studies. The polypeptide may be used to

CC identify modulators and ligands.

XX Sequence 337 AA;

SO Query Match 100.0%; Score 1785; DB 23 Length 337;

Best Local Similarity 100.0%; Pred. No. 1.5e-186

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLIIVGNFVAFVAVS 60

DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLIIVGNFVAFVAVS 60

QY 61 YFKALTPPTFFLLSLALADMFGLVLPSTIRSVESCFEFGDFLCRLHTYDTECLT 120

DB 61 YFKALTPPTFFLLSLALADMFGLVLPSTIRSVESCFEFGDFLCRLHTYDTECLT 120

QY 121 SIFHLCTSIDRHCALCDPLLPSPKFTVRALRIILAGMGVPAAYTSLFYTDDVERRLS 180

DB 121 SIFHLCTSIDRHCALCDPLLPSPKFTVRALRIILAGMGVPAAYTSLFYTDDVERRLS 180

QY 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCIMISLYKIEVVAIROAQOITTLTSL 240

DB 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCIMISLYKIEVVAIROAQOITTLTSL 240

QY 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

DB 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

QY 301 NPITIVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

DB 301 NPITIVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

RESULT 4

ABP56910

ID ABP56910 standard; Protein; 337 AA.

XX

AC ABP56910;

XX

DY 08-APR-2003 (first entry)

XX

DE Human orphan GPCR protein SEQ ID NO:2.

XX

KW Human: orphan G protein-coupled receptor; GPCR; 1NR; schizophrenia;

KW putative neurotransmitter receptor; transgenic mouse.

XX

OS Homo sapiens.

XX

PN WO2003001882-A2.

XX

PD 09-JAN-2003.

XX

XX 25-JUN-2002; 2002WO-US20269.

XX

PF 26-JUN-2001; 2001US-301281P.

XX

PR 14-DEC-2001; 2001US-340380P.

XX

XX (DELT-) DELTAGEN INC.

XX

PA Allen KD;

XX

PI WPI; 2003-201449/19.

XX

DR

DR N-PSDB; AB222929.

XX

PT Transgenic mice comprising disruptions in a putative neurotransmitter

PT receptor (PNR) gene, useful as models for studying diseases associated

PT with a disruption in a PNR gene, or for identifying agents for treating

PT schizophrenia

XX

PS Disclosure; Fig 2; 60pp; English.

XX

CC The present invention describes a transgenic mouse comprising a

CC disruption in a putative neurotransmitter receptor (PNR) gene, where

CC there is no native expression of endogenous PNR gene. PNR has

CC neuroleptic activity. The transgenic mice are useful as models for

CC studying diseases, disorders or conditions associated with phenotypes

CC relating to a disruption in a PNR gene. The transgenic mice and cells

CC comprising disruptions in PNR genes are also useful in evaluating

CC various treatments or identifying agents for treating disease states

CC in which PNR may be involved, such as schizophrenia. The present

CC sequence represents a human orphan G protein-coupled receptor which is

CC a PNR used in an example from the present invention.

XX

SO Sequence 337 AA;

Query Match 100.0%; Score 1785; DB 24; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.5e-186;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLIIVGNFVAFVAVS 60

DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLIIVGNFVAFVAVS 60

QY 61 YFKALTPPTFFLLSLALADMFGLVLPSTIRSVESCFEFGDFLCRLHTYDTECLT 120

DB 61 YFKALTPPTFFLLSLALADMFGLVLPSTIRSVESCFEFGDFLCRLHTYDTECLT 120

QY 121 SIFHLCTSIDRHCALCDPLLPSPKFTVRALRIILAGMGVPAAYTSLFYTDDVERRLS 180

DB 121 SIFHLCTSIDRHCALCDPLLPSPKFTVRALRIILAGMGVPAAYTSLFYTDDVERRLS 180

QY 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCIMISLYKIEVVAIROAQOITTLTSL 240

DB 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCIMISLYKIEVVAIROAQOITTLTSL 240

QY 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

DB 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

QY 301 NPITIVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

DB 301 NPITIVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

RESULT 5

ABB99760

ID ABB99760 standard; Protein; 337 AA.

XX

AC ABB99760;

XX

DY 24-MAR-2003 (first entry)

XX

DE Amino acid sequence of a protein 43% identical to human TA5 receptor.

XX

XX Human; trace amine receptor; TA5 receptor; G protein-coupled receptor;

KW GPCR; chromosome 6; haematological disorder; CNS disorder; asthma;

KW chronic obstructive pulmonary disease; COPD; cardiovascular disorder;

KW gastrointestinal disorder; cancer; diabetes; obesity;

XX

XX genitourinary disorder.

XX

OS Homo sapiens.

XX

PN WO200299107-A2.

XX

PD 12-DEC-2002.

XX

DR

XX 06-JUN-2002; 2002MO-EP06206.
PE
XX
XX 07-JUN-2001; 2001US-296136P.
PR
XX 17-APR-2002; 2002US-372809P.
PR
XX (FARB) BAYER AG.
PA
XX
XX
PI Zhu Z;
XX
XX WPI; 2003-140624/13.
DR
XX N-PSDB; AB233221.
XX
PT New polynucleotide encoding a G protein-coupled receptor polypeptide
PT useful for treating diseases, e.g. haematological, cardiovascular,
PT gastrointestinal or genitourinary disorders, asthma, cancer, diabetes
PT obesity -
PT
PS Disclosure; Page 153-154; 154pp; English.
XX
XX
CC The present sequence represents a protein which is 43% identical to a
CC human trace amine receptor designated TA5 receptor. TA5 is a
CC G protein-coupled receptor (GPCR), located on chromosome 6. TA5
CC polypeptides and polynucleotides are useful for the preparation of
CC a medicament for modulating the activity of the GPCR in a disease,
CC e.g. haematological disorders, a CNS disorder, chronic obstructive
CC pulmonary disease (COPD), asthma, a cardiovascular disorder, a
CC gastrointestinal disorder, cancer, diabetes, obesity or genitourinary
CC disorder.
XX
XX Sequence 337 AA;
XX

	Query Match	100.0%;	Score 1785;	DB 24;	Length 337;
	Best Local Similarity	100.0%;	Pred. No. 1.5e-186;		
	Matches 337;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1 MRAVFIOGAEBHPAAFCYOVNGSCPRTVHTLTGILVLYITCAAGMLIIVLGNVFAFAVS 60				
QY	61 YFKALHTPTNELLISLALADMFGLIVLPSTIRNSVSCWFFGDFLCRLHYLDLFLCIT 120				
Db	61 YFKALHTPTNELLISLALADMFGLIVLPSTIRNSVSCWFFGDFLCRLHYLDLFLCIT 120				
QY	121 SIFHLCFISIDRHOAICDPLLYPSKFTVAVLRYTLAGWGPAAATSLRXTDVTVERLS 180				
Db	121 SIFHLCFISIDRHOAICDPLLYPSKFTVAVLRYTLAGWGPAAATSLRXTDVTVERLS 180				
QY	181 QMLEEMPCVSGCQLLNKFWGMNFPLTFVYVCLIMISLYVILFVATRQAOOITLSSKL 240				
Db	181 QMLEEMPCVSGCQLLNKFWGMNFPLTFVYVCLIMISLYVILFVATRQAOOITLSSKL 240				
QY	241 AGAAKHERKAAKTIGIVGIYLCWLPETIDTWVDSLHETTPPLVEDIFTWFAVENSAC 300				
Db	241 AGAAKHERKAAKTIGIVGIYLCWLPETIDTWVDSLHETTPPLVEDIFTWFAVENSAC 300				
QY	301 NPILIVESYQERKALKITLSQKXSPQTRVVDLYQE 337				
Db	301 NPILIVESYQERKALKITLSQKXSPQTRVVDLYQE 337				

Accession	Protein Name	Gene Name	Species	Length (aa)	Weight (kDa)	PI	Ref
ABP81936	ABP81936 standard; Protein; 337 AA.		Human	337	36.5	5.2	1
XX	ABP81936;		Human	337	36.5	5.2	1
XX			Human	337	36.5	5.2	1
XX	04-MAR-2003 (first entry)		Human	337	36.5	5.2	1
XX			Human	337	36.5	5.2	1
DE	Human putative neurotransmitter receptor protein SEQ ID NO:356.		Human	337	36.5	5.2	1
XX			Human	337	36.5	5.2	1
KM	G protein-coupled receptor, GPCR; antigenic peptide; gene therapy;		Human	337	36.5	5.2	1
KW	G protein-coupled receptor modulator; antibody; Immune-related disease;		Human	337	36.5	5.2	1

XX	growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW	immunological-related disease; cell proliferative disease; autoimmune disease;
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; palm;
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.	
XX	
XX	Homo sapiens.
OS	
PN	WO200261087-A2.
XX	
PD	08-AUG-2002.
XX	
PF	19-DEC-2001; 2001WO-US50107.
XX	
PR	19-DEC-2000; 2000US-257144P.
XX	
PA	(LIFE-) LIFESPAN BIOSCIENCES INC.
PI	Burner GC, Roush CL, Brown JP;
XX	
DR	WPI; 2003-046718/04.
XX	
DR	N-PSDB; AB242784.
XX	
PT	New isolated antigenic peptides e.g., for G protein-coupled receptors
PT	(GPCR), useful for diagnosing and designing drugs for treating
PT	conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT	cancer Or autoimmune diseases -

CC The present invention describes antigenic peptides (1) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G-protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

	Query Match	Score	Length
Best Local Similarity	100.0%	1785	24
Matches	337	Conservative	0
		Mismatches	0
		Indels	0
		Gaps	0

QY 121 SIFHLCFISIDRHCAICDPLLPYSKFTVVALRYIILAGNCVPAAYTSLFLYDVTETRLS 180
 DB 121 SIFHLCFISIDRHCAICDPLLPYSKFTVVALRYIILAGNCVPAAYTSLFLYDVTETRLS 180
 QY 181 QMLEEPCVSCOLLNKFWMGNLNFLEFVPCIMISLVKIKIVVATROAQOITTLTSLKSL 240
 DB 181 QMLEEPCVSCOLLNKFWMGNLNFLEFVPCIMISLVKIKIVVATROAQOITTLTSLKSL 240
 QY 241 AGAAKHERKAAKTIGIVGIVYLWCWLPFTIDFWVDSLHFIIPPLVFDFIFMFAVFNSSAC 300
 DB 241 AGAAKHERKAAKTIGIVGIVYLWCWLPFTIDFWVDSLHFIIPPLVFDFIFMFAVFNSSAC 300
 QY 301 NPIIYFSTQWFRKALKLTLSQKVFSPQRTVDLYOE 337
 DB 301 NPIIYFSTQWFRKALKLTLSQKVFSPQRTVDLYOE 337

RESULT 7
 AAG65596
 ID AAG65596 standard; Protein; 321 AA.
 AC AAG65596;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human putative neurotransmitter receptor.
 XX
 KM G-protein coupled receptor; GPCR; human; therapeutic; gene therapy;
 KM neurotransmitter receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200172839-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09524.
 XX
 PR 27-MAR-2000; 2000US-192326P.
 PR 15-AUG-2000; 2000US-0637603.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Wang A, Cravchik A, Di Francesco V, Beasley EM;
 DR WPI; 2001-611615/70.
 XX
 PT New human G-protein coupled receptor, useful for identifying specific
 PT modulators, potential therapeutic agents, is related to the
 PT neurotransmitter receptor family -
 PS
 PS Disclosure: Fig 2; 63pp; English.

CC The invention provides a human G-protein coupled receptor (GPCR). The
 CC GPCR is useful as target for identifying specific modulators and
 CC binding agents, potentially useful as human therapeutic agents, and
 CC especially for control of diseases in which GPCR is implicated, and for
 CC production of specific antibodies (Ab), or to elicit other immune
 CC responses. GPCR may be used as reagents for determination of the level
 CC of GPCR or its binding partners, as tissue marker, as therapeutics and
 CC for pharmacogenomic studies. Ab are useful for isolation and purification
 CC of GPCR, and for determination of GPCR, in diagnosis and monitoring. Ab
 CC can be used in pharmacogenomic analysis, for tissue typing, and as
 CC therapeutic modulators of GPCR. GPCR nucleic acids are useful for
 CC recombinant expression of the protein, and as source of primers and
 CC probes (for diagnosis) and of antisense sequences and ribozymes (for
 CC therapy). They can be used for identifying modulators of its expression,
 CC monitoring gene expression during therapy, identifying mutations in the
 CC GPCR-encoding gene, construction of gene therapy vectors and preparing
 CC transgenic animals, used to study function of GPCR and to identify
 CC modulators. The present sequence represents a human putative
 CC neurotransmitter receptor.

XX SQ Sequence 321 AA;
 Query Match 95.4%; Score 1703; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-177;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CYOVNCSCEPTVHTLGIQVLYITLCAAGMLIYLGWVFAVAFYFKALHTPPNFTLLST 76
 DB 1 CYOVNCSCEPTVHTLGIQVLYITLCAAGMLIYLGWVFAVAFYFKALHTPPNFTLLST 60
 QY 77 ALADNMLGLVLPSTIRSYSCWFGDFLCRIHTLIDLPCLTSIFHLCFISIDRHCAI 136
 DB 61 ALADNMLGLVLPSTIRSYSCWFGDFLCRIHTLIDLPCLTSIFHLCFISIDRHCAI 120
 QY 137 CDPLLPYSKFTVVALRYIILAGNCVPAAYTSLFLYDVTETRLSOMLEEPCVSCOLL 196
 DB 121 CDPLLPYSKFTVVALRYIILAGNCVPAAYTSLFLYDVTETRLSOMLEEPCVSCOLL 180
 QY 197 NKEFWMLNPLFEPVPCIMISLVKIKIVVATROAQOITTLTSLKSLAGAAKHERKAAKTIGI 256
 DB 181 NKEFWMLNPLFEPVPCIMISLVKIKIVVATROAQOITTLTSLKSLAGAAKHERKAAKTIGI 240
 QY 257 VGCITLWCWLPFTIDFWVDSLHFIIPPLVFDFIFMFAVFNSSACNPIIYFSTQWFRKAL 316
 DB 241 VGCITLWCWLPFTIDFWVDSLHFIIPPLVFDFIFMFAVFNSSACNPIIYFSTQWFRKAL 300
 QY 317 KLTLSQKVFSPQRTVDLYOE 337
 DB 301 KLTLSQKVFSPQRTVDLYOE 321

RESULT 8
 ABJ37891
 ID ABJ37891 standard; Protein; 339 AA.
 AC ABJ37891;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE NOVX protein sequence SEQ ID NO 28.

XX KM Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
 KM vulnerable; virucide; antibacterial; protozoacide; fungicide; nootropic;
 KM antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
 KM anticonvulsant; antidiabetic; analgesic; dermatological; keratolytic;
 KM antiseborrheic; antirheumatic; antiarthritic; antiinflammatory; anti-HIV;
 KM cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
 KM antidiarr; anorectic; antidiabetic; antiallergic; haemostatic;
 KM neuroleptic; antidepressant; antinfertility; NOVX; human disease;
 KM NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
 KM parasitic infection; Alzheimer's disease; stroke; forensic biology;
 KM immunogen; non-human transgenic animal; gene therapy.

XX OS Unidentified.
 XX
 PN WO200281517-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 22-JAN-2002; 2002WO-US02064.
 XX
 PR 19-JAN-2001; 2001US-262892P.
 PR 23-JAN-2001; 2001US-263598P.
 PR 24-JAN-2001; 2001US-263799P.
 PR 25-JAN-2001; 2001US-264117P.
 PR 25-JAN-2001; 2001US-264139P.
 PR 26-JAN-2001; 2001US-264478P.
 PR 30-JAN-2001; 2001US-263351P.
 PR 02-MAR-2001; 2001US-272870P.
 PR 14-MAR-2001; 2001US-275927P.
 PR 14-MAR-2001; 2001US-275990P.
 PR 15-MAR-2001; 2001US-276449P.

PR 20-MAR-2001; 2001US-277358P.
 PR 23-MAR-2001; 2001US-278151P.
 PR 29-MAR-2001; 2001US-279857P.
 PR 20-APR-2001; 2001US-285140P.
 PR 20-APR-2001; 2001US-285141P.
 PR 17-MAY-2001; 2001US-287484P.
 PR 10-JUN-2001; 2001US-291701P.
 PR 08-JUN-2001; 2001US-296960P.
 PR 10-JUL-2001; 2001US-304353P.
 PR 10-JUL-2001; 2001US-304355P.
 PR 12-JUL-2001; 2001US-304866P.
 PR 09-AUG-2001; 2001US-311289P.
 PR 13-AUG-2001; 2001US-311975P.
 PR 16-AUG-2001; 2001US-312937P.
 PR 18-OCT-2001; 2001US-330227P.
 PR 29-NOV-2001; 2001US-334198P.
 XX (CURA-) CURAGEN CORP.
 PA
 PI Decristofaro MF, Padigaru M, Miller C, Tchernev V, Zhong H;
 PI Zhong M, Anderson D, Ballinger R, Gerlach V, Splek KA;
 PI Rastelli L, Kekuda R, Guo X, Zernusen B, Andrew D, Mezes P;
 PI Patuvarajan M, Burgess CE, Eisen A, Molenc A, Baumgartner J;
 PI Shumkets RA, Gusev V, Vernet CAM, Taupier RJ, Pena C, Shenoy S;
 PI Li L, Caseman S, Boldog F, Fernandes E, Smithson G, Malyankar U;
 PI Tallion B, Liu X;
 XX
 XX WPI: 2003-058504/05.
 DR N-PSDB: ABT33356.
 XX
 PT New polypeptides, designated as NOVX, useful for diagnosing and
 PT treating infections, neurological diseases, cancer, allergy, and bone,
 PT immunological, skin, renal, brain, muscle and autoimmune disorders -
 XX
 XX Claim 1; Page 83; 672pp: English.
 XX
 CC The invention relates to a novel isolated polypeptide, designated NOVX
 CC (NOV1 - 33), consisting of a mature form of one of 61 sequences, given
 CC in the specification, or its variant, where amino acid residue(s) in the
 CC variant differ from the mature form, provided that the variant differs
 CC in not more than 15 % of the amino acids from the sequence of the mature
 CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
 CC an antibody to the polypeptides, are useful for treating or preventing a
 CC NOVX-associated disorder in humans and for treating a syndrome associated
 CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
 CC the encoding nucleic acids, are useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOVX
 CC polypeptide and polynucleotide, by measuring the level of polypeptide
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. NOVX
 CC polypeptide is also useful for identifying an agent that binds to NOVX
 CC and a cell expressing NOVX is useful for identifying an agent that
 CC modulates the expression or activity of NOVX. The antibodies and a
 CC polypeptide having 95 % sequence identity to NOVX polypeptides are useful
 CC for treating a pathological state in a mammal. The antibodies are also
 CC useful for determining the presence or amount of NOVX in a sample. NOVX
 CC polypeptides, polynucleotides and antibodies specific for the
 CC polypeptides are useful for treating or preventing disorders or syndromes
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
 CC infections. They can also treat disorders such as e.g., Alzheimer's
 CC disease or a stroke. The NOVX encoding nucleic acids are useful for
 CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
 CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
 CC for identifying a cell or tissue type in a biological sample, to amplify
 CC DNA sequences from very small biological samples such as tissues e.g.
 CC hair or skin or body fluids in forensic biology and as primers and probes
 CC for use in identifying and/or cloning NOVX homologues in other cell
 CC types. The NOVX proteins are useful as an immunogen to generate
 CC antibodies which are useful for diagnostically monitoring protein levels
 CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
 CC useful for producing non-human transgenic animals which are useful for
 CC studying the function and/or activity of NOVX protein and for identifying
 CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic

CC acids can be used in gene therapy. This sequence represents a NOVX
 CC protein of the invention.
 XX
 SQ Sequence 339 AA:
 Query Match 45.5%, Score 812.5; DB 24; Length 339;
 Best Local Similarity 46.1%, Pred. No. 3.8e-80;
 Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3;
 OY 17 CYQ-VNGSCPTVHTIGIOLIVYLCAAGMLIITLGNVFAVAFYFALHTPTNFIILS 75
 DB 5 CYKVNESCITPTPSGPRSLIVAVLFGAVLAAPGNLVAITLHFRQLHTPTNFIILAS 64
 OY 76 IALADMEGLDLVPLSTIRSVESQWFGDFCLRLHTYLDLFCULSIFHLCFISIDRRCA 135
 DB 65 IACADELVGVTVMPFSTVRSVESCWYEGDSYCKRHTCDTSFCFASLFLHCCISVDRIA 124
 OY 136 ICDPLVPSKFTTVVALRYILAGCVPAAYVSLFLYDVVETRLSQMLEMPVCGSQQL 195
 DB 125 VTDPLVPTKFTVSVSGICIVLSWFFSVTSFSIFYGANEGIEELVALTCVGGCOAP 184
 OY 196 LNKFMGMLNPLFVPCILMISLVKIFPVVTRBOAOI-TTLRSIAGA-----AKHE 247
 DB 185 LNQMWVLCFLFLFPNVAMVFTSKITFLVAKHQARKIESTASQAQSSSEYKERVAKRE 244
 OY 248 RKAATIGIVGIVLCLMPTPTIDMVDLSLHFTTPPLVFDIETFMFAVFNACNPITVVF 307
 DB 245 RKAATIGIAMAALVSLPFLYDAVIDAYNFTTPPVYELVWCYYNSAMPLIYAF 304
 OY 308 SYQWFRKAKLTLSQKVFSPQRTVDXOE 337
 DB 305 FYQWFGKAIKLIVSGKVLRTDSTTNLFSF 334
 RESULT 9
 AAB18764
 ID AAB18764 standard; Protein: 348 AA.
 XX
 AC AAB18764;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of the human SNORF1 receptor.
 XX
 KW SNORF1 receptor; Inflammation; arthritis; autoimmune disease;
 KW transplant rejection; Infection; AIDS; pain; psychotic disorder;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT 33..58 Location/Qualifiers
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 67..88
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 111..128
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 148..169
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 198..224
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 236..280
 FT /note= "putative transmembrane domain"
 FT Domain
 FT 293..318
 FT /note= "putative transmembrane domain"
 XX
 PN US6117990-A.
 XX
 PD 12-SEP-2000.
 XX
 PD 06-APR-1999; 99US-0286805.
 XX
 PF 06-APR-1999; 99US-0286805.
 XX
 PR 06-APR-1999; 99US-0286805.

XX (SYNA-) SYNAPTIC PHARM CORP.
 PA Bonini JA, Borowsky BE;
 XX WPI: 2000-610854/58.
 DR N-PSDB: AAA75824.
 XX
 PT New recombinant nucleic acid molecules, with sequences identical to the
 PT human and rat SNORF1 receptor-encoding nucleic acid molecules and
 PT possessing the structural motif characteristics of a G-protein -
 XX
 PS Disclosure: Fig 2A-B; 19pp; English.
 XX
 CC The present sequence represents a SNORF1 receptor. The SNORF1 nucleic
 CC acids may be used as probes to obtain homologous nucleic acids from other
 CC species and to detect the existence of nucleic acids having complementary
 CC sequences in samples. The nucleic acids may also be used to express the
 CC receptors they encode in transfected cells. Also, use of the receptor
 CC encoded by the SNORF1 receptor nucleic acid sequence enables the
 CC discovery of the endogenous ligand and to elucidate the role of the
 CC SNORF1 receptor. The receptor may be employed for designing drugs for
 CC treating various pathological conditions such as chronic and acute
 CC inflammation, arthritis, autoimmune diseases, transplant rejection,
 CC bacterial and fungal infections, AIDS, pain, psychotic and neurological
 CC disorders. Transfected cells with the receptor may be used to test
 CC compounds which bind to the receptor and which activate or inhibit the
 CC functional responses.
 CC
 XX
 SQ Sequence 348 AA:
 Query Match 45.5%; Score 812.5; DB 21; Length 348;
 Best Local Similarity 46.1%; Pred. No. 3.9e-80;
 Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3;
 QY 17 CYQ-VNGSCPRTVHTLGIGLVYITLCAAGMLIIVGNVAVAVSYFKAHPTPTNLLS 75
 DB 14 CKNVNESCIKTPYSPGPRISIIYAVLGFSAVLAAGNLVMTAILHFKQLHTPTNPLAS 73
 QY 76 LALADMFLGLVLPSTIRSVESCFEGDFLCRLHTYDLPCLTISIFHLCTSIDRHA 135
 DB 74 LACADFLVGVTVMPSTVRSVSCWYFGDSYCKFHCFTSPSCFASLFLHCISVDRYIA 133
 QY 136 ICDPLLYPSKFTVRAVALRIITLAGMGVPAAYTSLEFYTVDVETRLSOMLEMPVSCQLL 195
 DB 134 VTDPLTYPTKFTVSVSGICIVLSWFFSVYSSIFVTGANESGIEELVALTCVGGCQAP 193
 QY 196 LKRFMGWLNPLFEVPCIMISLYKIFVAVTRAOOI-TTLKSLAGA-----AKHE 247
 DB 194 LNONVNLCLFLFIPNVAMVFIYSKIFVAHQAKISTASQOSSSESEKERYAKKE 253
 QY 248 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPITTYE 307
 DB 254 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPITTYE 313
 QY 308 STQWRKAKLTLTSLQKVSFSPOTRYVDLYOE 337
 DB 314 FYQWFGKAIKILIVSGKVLMTDSSSTNLESE 343
 RESULT 10
 ID ABB98168 standard; Protein; 348 AA.
 AC ABB98168;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human AXOR 106 amino acid sequence.
 XX
 KW AXOR 106; GPCR; G-Protein Coupled receptor; antihistaminic; antifungal;
 KW antitumor; antiprotocole; anti-HIV; analgesic; cytostatic; antidiabetic;
 KW anorectic; anabolic; antilastmatic; antiparkinsonian; cardiast;

KW hypertensive; hypotensive; diuretic; osteopathic; antianginal;
 KW cerebroprotective; antitumor; antiallergic; human; bacterial; fungal;
 KW protozoan; viral; infection; human immunodeficiency virus; HIV-1;
 KW HIV-2; pain; cancers; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW stroke; ulcer; allergy; vaccine; screening; GPR57.
 XX
 OS Homo sapiens.
 XX
 PN GB2372249-A.
 XX
 PD 21-AUG-2002.
 XX
 PF 18-OCT-2001; 2001GB-0025067.
 XX
 PR 20-OCT-2000; 2000US-242399P.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Shabon U, Elshourbagy N, Agarwal P, Quillen JW, Gattu M;
 DR WPI: 2002-610876/66.
 DR N-PSDB: ABQ79377.
 XX
 PT New G-protein coupled receptor protein, useful for developing
 PT diagnostic reagents and for treating viral infections, pain, cancers,
 PT diabetes, and development of vaccines -
 XX
 PS Claim 1 (c); Page 30; 37pp; English.
 XX
 CC The invention relates to a polypeptide designated AXOR, which is a member
 CC of the G-protein coupled 7 trans-membrane receptor family. The activity
 CC of the polypeptide of the invention may be described as, antibacterial,
 CC antifungal, antiviral, antiprotocole, anti-HIV, analgesic, cytostatic,
 CC antidiabetic, anorectic, anabolic, antilastmatic, antiparkinsonian,
 CC cardiant, hypertensive, hypotensive, diuretic, osteopathic, antianginal,
 CC cerebroprotective, antitumor and antiallergic. Polynucleotides of the
 CC invention can be used to treat diseases including bacterial, fungal,
 CC protozoan and viral infections, human immunodeficiency virus, (HIV-1,
 CC HIV-2), pain, cancers, diabetes, obesity, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, and allergies. Polypeptides and polynucleotide may also
 CC be used in vaccines. The polypeptide may be used in low capacity
 CC screening methods and also in high-throughput screening formats. The
 CC current sequence represents the AXOR 106 amino acid sequence.
 CC
 XX
 SQ Sequence 348 AA:
 Query Match 45.5%; Score 812.5; DB 23; Length 348;
 Best Local Similarity 46.1%; Pred. No. 3.9e-80;
 Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3;
 QY 17 CYQ-VNGSCPRTVHTLGIGLVYITLCAAGMLIIVGNVAVAVSYFKAHPTPTNLLS 75
 DB 14 CKNVNESCIKTPYSPGPRISIIYAVLGFSAVLAAGNLVMTAILHFKQLHTPTNPLAS 73
 QY 76 LALADMFLGLVLPSTIRSVESCFEGDFLCRLHTYDLPCLTISIFHLCTSIDRHA 135
 DB 74 LACADFLVGVTVMPSTVRSVSCWYFGDSYCKFHCFTSPSCFASLFLHCISVDRYIA 133
 QY 136 ICDPLLYPSKFTVRAVALRIITLAGMGVPAAYTSLEFYTVDVETRLSOMLEMPVSCQLL 195
 DB 134 VTDPLTYPTKFTVSVSGICIVLSWFFSVYSSIFVTGANESGIEELVALTCVGGCQAP 193
 QY 196 LKRFMGWLNPLFEVPCIMISLYKIFVAVTRAOOI-TTLKSLAGA-----AKHE 247
 DB 194 LNONVNLCLFLFIPNVAMVFIYSKIFVAHQAKISTASQOSSSESEKERYAKKE 253
 QY 248 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPITTYE 307
 DB 254 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPITTYE 313
 QY 308 STQWRKAKLTLTSLQKVSFSPOTRYVDLYOE 337
 DB 314 FYQWFGKAIKILIVSGKVLMTDSSSTNLESE 343

Dd		254 RKAAKTLGIAMAFELVSMPLVDVAIDAYNMFIIPPVEILWCVYNSANMLPIIYA F 313
Oy		308 STQMFRAKALKLISGVESPQRRTDYDIOE 337 : : :
Dd		314 FYWMFGKAIKLIYSGRVLNTRDSSTYNLTFSE 343
		RESULT_11
ID	ABP81735 standard; Protein; 348 AA.	
XX		
AC	ABP81735;	
DE	04-MAR-2003 (first entry)	
DT		
XX	Human trace amine receptor 3 protein SEQ ID NO:645.	
DE		
KM	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related diseases; cell regeneration-related diseases; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.	
KW		
KX	Homo sapiens.	
OS		
NN	M0200261087-AZ.	
PJ	08-AUG-2002.	
PD		
PN	19-DEC-2001; 2001MO-US50107.	
PF	19-DEC-2000; 2000US-257144P.	
PR	(LIFE-) LIFESPAN BIOSCIENCES INC.	
PS	Burmer GC, Roush CL, Brown JP.	
PT	WI: 2003-046718/04.	
XX	N-PDB: ABZ42581.	
DR	New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases	
XX	Disclosure; Fig 1; 523pp; English.	
CC	The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, arterosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, hypertension,	

CC		hypertension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC		any other disorder in which GPCRs are involved. The antibodies may be
CC		used in immunosassays and immunodiagnosis. AB242523 to AB24269 encode
CC		GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC		exemplification of the present invention.
XX		
SO	Sequence	348 AA;
Query Match	45..58; Score 812.5; DB:24; Length 348;	
Best Local Similarity	46.18; Pred. No. 3.9e-80;	
Matches 152;	Conservative 64; Mismatches 105; Indels 9; Gaps 3.	
OY	17 CYQ-VNSSCPTVTWTLGIQLIYLTCAGAMLIILGNGVFAVAVSYFKALHTPTNELLIS	75
Dd	14 CYNKVNSSCIKTIPYSPGRSLIVAVLGSGANLAFGNLTVMIALIHFKQLHTPTNELIAS	73
OY	76 LAILADMLGLILVPLSTIRSVESCGWFQDFLCRLHTYLDTLFCLTSLTHLCFISIDRHCA	135
Dd	74 LACADFVLGVVMPFSYTVRSVESGWFPDASCKFHCTCDTSFCFASLSLHLCISIDRYIA	133
OY	136 ICDPLLYPSKFTVNVVALRYILIAGCWPAARYSLFLYTDVVESTRLSQMLEEMPCVSCOLL	195
Dd	134 VTDLPLYPTKRTTYSVSGICIVLSMFFSVTYSEFSITFYTGANEGLIELVALLCVGCCAP	193
OY	196 LNRKWGMNLNPFLTFVPCLLIMISLYKTFVATROAQI-TLSKSLAGA-----AKHE	247
Dd	194 LNQMWWVLICFLDFEIPNVAMVFISKIFLVAKHQARKIESVASQAOSSESSEYKERVARKE	253
OY	248 RKAATGTIGVVGIIILCMLPTTIIDTPMWSLHPTPIPLPFIEFIFAVANSNCNIITYVF	307
Dd	254 RKAAKTGTIGMAAALVLSWLPVLVDVAVIDAYNMFTTPPIYVELLWCYYINSMANPLIYAF	313
OY	308 SYQMFRAKLITLSQKVFPSPOTFRVDLYQE	337
Dd	314 FYQMFGRKAIKLIVSGKVLRTDSSTTNLFSE	343
RESULT_12		
AAB18765		
ID	AAB18765 standard; Protein; 338 AA.	
XX		
XX	AAB18765;	
DT	22-JAN-2001 (first entry)	
DE	Amino acid sequence of the rat SNORF1 receptor.	
XX		
KW	SNORF1 receptor; inflammation; arthritis; autoimmune disease;	
RW	transplant rejection; infection; AIDS; pain; psychotic disorder;	
XX	neurological disorder.	
XX		
OS	Rattus norvegicus.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	23..48
FT	/note= "putative transmembrane domain"	
FT	Domain	57..78
FT	/note= "putative transmembrane domain"	
FT	Domain	101..118
FT	/note= "putative transmembrane domain"	
FT	Domain	138..159
FT	/note= "putative transmembrane domain"	
FT	Domain	188..214
FT	/note= "putative transmembrane domain"	
FT	Domain	246..270
FT	/note= "putative transmembrane domain"	
FT	Domain	283..308
FT	/note= "putative transmembrane domain"	
XX		
PX	US6117990-A.	
XX		
DD	12-SEP-2000.	
XX		

PF 06-APR-1999; 9905-0286805.
 XX 06-APR-1999; 9905-0286805.
 XX (SYNA-) SYNAPTIC PHARM CORP.
 PI Bonini JA, Borowsky BE;
 DR WPI: 2000-610854/58.
 DR N-PSDB; AAA75825.
 XX
 PT New recombinant nucleic acid molecules, with sequences identical to the
 PT human and rat SNORF1 receptor-encoding nucleic acid molecules and
 PT possessing the structural motif characteristics of a G-protein
 PS Disclosure; Fig 4A-B; 19pp; English.
 XX
 CC The present sequence represents a SNORF1 receptor. The SNORF1 nucleic
 CC acids may be used as probes to obtain homologous nucleic acids from other
 CC species and to detect the existence of nucleic acids having complementary
 CC sequences in samples. The nucleic acids may also be used to express the
 CC receptors they encode in transfected cells. Also, use of the receptor
 CC encoded by the SNORF1 receptor nucleic acid sequence enables the
 CC discovery of the endogenous ligand and to elucidate the role of the
 CC SNORF1 receptor. The receptor may be employed for: designing drugs for
 CC treating various pathological conditions such as chronic and acute
 CC inflammation, arthritis, autoimmune diseases, transplant rejection,
 CC bacterial and fungal infections, AIDS, pain, psychotic and neurological
 CC disorders. Transfected cells with the receptor may be used to test
 CC compounds which bind to the receptor and which activate or inhibit the
 CC functional responses.
 CC
 XX
 SQ Sequence 338 AA;
 Query Match 44.6%; Score 795.5; DB 21; Length 338;
 Best Local Similarity 45.5%; Pred. No. 2.7e-78;
 Matches 150; Conservative 64; Mismatches 107; Indels 9; Gaps 3;
 QY 17 CYQ-VNGSCPRTVHTGIDLVYITCAAGMLITVIGNVEAFANVSFKALHTPTNLLLS 75
 DB 4 CVENVNGSCIKSSYSWMPRAILYAVLGALMLAVFENLLVITAILHPKQHTPTNLLVAS 63
 QY 76 LALADMFGLVLPSTIRSVESCFEGDFLCRLHTYLDI LFCULTSIFHLCTSIDRCA 135
 DB 64 LACADFLVGVTVAFVSVSECVGFCGYCFHCFCFDI SFCFASLFIHLCCISIDRYVA 123
 QY 136 ICDDPLYPKSFYRVNLTARTIAGMGVPAVTSILFTDV EHTLSQMLEMPGVSGQLL 195
 DB 124 VDDPLTYPTKFTISVSGVCIASWFSVTYSISFTIGAEBCIEELVVALTCVGCQAP 183
 QY 196 LKFMGMNFPLEFVPCILMISLYKIFVAVFRAQOIT- TLKSLAGA-----AKHE 247
 DB 184 LQNVNVLFCFLFELPVVAVFLYGRILYLAQKQARKIEK SANQPASSSYKERVARE 243
 QY 248 KRAAKTLGIVGVIYLCMLPFTIDWVDSILHTITPPLVDITIMAFYNSACNPITTYF 307
 DB 244 RRAAKTLGIAAMAFVLSMPLIIDAVIDAYMNTIPAYY EILVMCVYNSANPLIYAF 303
 QY 308 SYOMFRKALKLTSOKVFSPOTRTVLYOHE 337
 DB 304 FYWFRKAIKLIYSGVFRADSRITLSE 333
 RESULT 13
 ID AAG80970 standard; protein; 345 AA.
 AC AAG80970;
 XX
 DT 28-AUG-2001 (first entry)
 XX
 DE Human nGPCR40 #2.
 XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 XX
 OS Homo sapiens.
 PN W0200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000MO-US31581.
 XX
 PR 16-NOV-1999; 9905-0165838.
 PR 17-NOV-1999; 9905-0166071.
 PR 19-NOV-1999; 9905-0166678.
 PR 28-DEC-1999; 9905-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185530.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PNA) PHARMACIA & UPJOHN CO.
 PI Vogel I G, Wood LS, Parodi LA, Hiesch RR, Land P, Slightom J;
 PI Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
 DR WPI: 2001-389826/41.
 DR N-PSDB; AAH51010.
 XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 XX
 PS Claim 37; Page 91; 26pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is one such G protein-coupled receptor. GPCRs are also known as
 CC seven transmembrane receptors and function in signal transduction. The
 CC nGPCR coding sequences are useful for screening a human to diagnose a
 CC disorder affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease.
 XX
 SQ Sequence 345 AA;
 Query Match 44.1%; Score 786.5; DB 22; Length 345;
 Best Local Similarity 44.2%; Pred. No. 2.7e-77;

Search completed: August 26, 2003, 14:23:51
Job time : 46 secs

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XX OS Homo sapiens.
XX PN WO200261075-A1.
XX PD 08-AUG-2002.
XX PF 31-JAN-2002; 2002WO-JP00773.
XX PR 01-FEB-2001; 2001JP-0025037.
XX PR 30-MAR-2001; 2001JP-0102559.
XX PR 04-APR-2001; 2001JP-0105435.
XX PA (TAKEDA ) TAKEDA CHEM IND LTD.
XX PI Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;
XX N-PSDB: ABO74527, ABO74530.
XX DR WPI: 2002-608518/65.
XX DR N-PSDB: ABO74527, ABO74530.
XX PT G-protein coupled receptor protein expressed in human kidney for design
XX PT of drugs and reagents for treatment and diagnosis of a broad range of
XX PT diseases including cancer -
XX PS Claim 1, Fig 2, 106pp; Japanese.
XX
CC The present sequence represents a human G protein-coupled receptor
CC protein designated TGR36 (1), which is expressed in human kidney. (1)
CC has nootropic, neuroleptic, vasotropic, hypotensive, antiinflammatory,
CC antidiabetic, immunosuppressive, antiviral, antibacterial, nephrotropic
CC and cytoskeletal activities, and can be used in the modification or
CC inhibition of signal transmission mediated by TGR31 and associated with
CC a broad range of disorders. (1) is useful for treatment, prevention and
CC diagnosis of central nervous system diseases (such as Alzheimer's
CC disease, anorexia and dementia), metabolic diseases (such as diabetes
CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian
CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),
CC circulatory diseases (such as hypertension, atherosclerosis and angina),
CC inflammatory diseases (such as allergy and rheumatism), respiratory
CC diseases (such as asthma and bronchitis), digestive diseases (such as
CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune
CC diseases), and infections (such as AIDS, pneumonia and influenza).
XX
SQ Sequence 345 AA:
Query Match 44.1%; Score 786.5; DB 23: Length 345;
Best Local Similarity 44.2%; Pred. No. 2,7e-77;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;
QY 17 CY-QVNGSCPRTVHTLQIQLVYLTCAGMLIVLGNVFAFVAVSYKALHTPTNELLLS 75
DB 14 CYANVNGSCVKIPFSGSRVILIVFGFVAVLAVFGLNLWMISILHFKQLHSPTNPLVAS 73
QY 76 LALADMFGLVLPSTISVSQCFGDFLCRLHTYLDLFLCTISIFHLCTSIDRHCA 135
DB 74 LACADFLVGVTVAFPMVTRVESCWFSGFCTCCDVAFCYSSLFHLCTSIDRYIA 133
QY 136 ICDPLLYPSKFTVRAVLRYLWGMVPAVYSLFLYTDVETRLSQMLEMPCVSGCOLL 195
DB 134 VTDPLVYPTKFTVSVSGICISWILPLMTSGAVFTTGYDGLLEELSDALNCTIGGQTV 193
QY 196 LKFWGMNPLFEVPCILMISLYKIFVAVRQAOOI-TTLRSK-----LAGAKHE 247
DB 194 VNQNMVLTDFLSPFIPTIMILYGNIPVARQAKIEWTSGKTESSESSEYKARVARE 253
QY 248 RRAAKTLGIVNGIYLLCWPFTIDMVDSILHFTIPPLVFDITWFAFNSACNPITTYF 307
DB 254 RRAAKTLGIVVAFEMLSLPSIDSILDAFMGFTIPACIYEICCCWCAYYNSANPLIYAL 313
QY 308 SYOMFRKALKLTSOKVFSFQRTVVDLYOE 337
DB 314 FYFWFRKALKIVITGOVLKNSATMNLFS 343

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:22:32 ; Search time 19 seconds
(without alignments)
1705.729 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785

Sequence: 1 MRAVFIOGAEEHPAFCYQV.....ITLSQVTSPTQTVLYXOE 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76:***
2: PIR2:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	337	2	JCS5832
2	446.5	25.0	387	2	S55550
3	446.5	25.0	406	2	S55549
4	420	23.5	359	2	JC4120
5	419	23.5	515	2	A40491
6	418	23.4	517	2	A45121
7	417	23.4	483	2	A25896
8	416.5	23.3	358	2	JQ1278
9	415.5	23.3	359	2	JH0449
10	413.5	23.2	477	2	S71323
11	412.5	23.1	429	2	S65656
12	412.5	23.1	466	2	JN0765
13	412.5	23.1	466	2	S36794
14	412.5	23.1	499	2	I57959
15	411	23.0	465	2	S65657
16	409.5	22.9	465	2	I51661
17	408	22.9	515	2	JC1525
18	407.5	22.8	374	2	I77467
19	404.5	22.7	436	2	JN0591
20	404.5	22.7	466	2	S36794
21	404	22.6	377	2	B30341
22	401.5	22.5	437	2	I57942
23	400	22.4	464	2	S12591
24	398.5	22.3	359	2	A35008
25	398.5	22.3	363	2	I50475
26	397.5	22.3	459	2	A56849
27	397	22.2	440	2	JC5520
28	396.5	22.2	377	2	A53279
29	394.5	22.1	428	2	A55044

30	393.5	22.0	446	1	DYH0D1	dopamine receptor
31	393	22.0	377	2	S68423	serotonin receptor
32	393	22.0	457	2	I51660	dopamine D1B recep
33	392.5	22.0	444	2	C55886	dopamine receptor
34	392	22.0	451	2	I51659	dopamine D1A recep
35	391.5	21.9	463	2	B56849	dopamine receptor-
36	390.5	21.9	418	2	S00260	beta-2-adrenergic
37	390	21.8	477	1	ORH0B1	beta-1-adrenergic
38	388	21.7	476	2	JC5042	G protein-coupled
39	387.5	21.7	446	2	I47217	dopamine receptor
40	387	21.7	450	2	A55886	dopamine receptor
41	387	21.7	450	2	A38316	alpha-2-adrenergic
42	386.5	21.7	389	2	S68422	serotonin receptor
43	386	21.6	390	2	JN0268	serotonin receptor
44	385.5	21.6	390	2	S58126	serotonin receptor
45	385.5	21.6	418	2	S10855	beta-2-adrenergic

ALIGNMENTS

RESULT 1

JCS5832 neurotransmitter receptor - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999

C:Accession: JCS5832

R:Zeng, Z.; Fan, P.; Rand, E.; Kyaw, H.; Su, K.; Madlike, V.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 242, 575-578, 1998

A:Title: Cloning of a putative human neurotransmitter receptor expressed in skeletal

A:Reference number: JCS5832; MUID:98125534; PMID:9464258

A:Accession: JCS5832

A:Molecule type: mRNA

A:Residues: 1-337 <REN>

A:Cross-references: GB:AF021818; NID:92465431; PIDN:AAC39581.1; PID:92465432

A:Experimental source: brain

C:Genetics:

A:Map position: 6q23

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; receptor; transmembrane protein

F:29-63/Domain: transmembrane #status predicted <TM1>

F:69-95/Domain: transmembrane #status predicted <TM2>

F:114-118/Domain: transmembrane #status predicted <TM3>

F:149-173/Domain: transmembrane #status predicted <TM4>

F:186-200/Domain: transmembrane #status predicted <TM5>

F:204-229/Domain: transmembrane #status predicted <TM6>

F:253-310/Domain: transmembrane #status predicted <TM7>

F:21/Binding site: cardhygrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1785; DB 2; Length 337;

Best local Similarity 100.0%; Pred. No. 4,6e-143;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRAVFIOGAEEHPAFCYVNGSCPRTVHTLGIVLYITCAAGMLIIVGNVFAVAVS 60
DB	1	MRAVFIOGAEEHPAFCYVNGSCPRTVHTLGIVLYITCAAGMLIIVGNVFAVAVS 60
QY	61	YFKAHTPTNFTLSTALADMTGLVLPSTIRSVESQWFGDFLCRHATYIDTFLFCT 120
DB	61	YFKAHTPTNFTLSTALADMTGLVLPSTIRSVESQWFGDFLCRHATYIDTFLFCT 120
QY	121	SIFHLCFISIDRHCACDPLLYPSKFTVVALRYIILAGGVPAAYSLFLYDVVETRSL 180
DB	121	SIFHLCFISIDRHCACDPLLYPSKFTVVALRYIILAGGVPAAYSLFLYDVVETRSL 180
QY	181	QMLEEPCVGSQCLLNKFWGMLNPLFFVPCILMISLYKIFVATROAQDITTLKSL 240
DB	181	QMLEEPCVGSQCLLNKFWGMLNPLFFVPCILMISLYKIFVATROAQDITTLKSL 240
QY	241	AGAAKHERKAATIGIVGIVYLLCMLPFTIDPVMSLHPTIPVDFEITFAVFNASC 300
DB	241	AGAAKHERKAATIGIVGIVYLLCMLPFTIDPVMSLHPTIPVDFEITFAVFNASC 300

OY 301 NPIIVFSGMFKKALTLTSLQKVSQPTRTDLYOE 337
 |||||
 DB 301 NPIIVFSGMFKKALTLTSLQKVSQPTRTDLYOE 337

RESULT 2

5-HT4S receptor - rat
 S55550
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
 C:Accession: S55550
 R:Gerald, C.; Adham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.;
 EMBO J. 14, 2806-2815, 1995
 A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization of
 A:Reference number: S55549; MUID:95317299; PMID:7796807
 A:Accession: S55550
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-387 <GER>
 A:Cross-references: GB:020906; NID:9244638; PIDN:AAC52232.1; PID:9244639
 C:Superfamily: vertebrate rhodopsin

Query Match 25.0%; Score 446.5; DB 2; Length 387;
 Best Local Similarity 33.1%, Pred. No. 3.5e-30;
 Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

OY 33 IQLVLYLT-CAAGMLIIVLGNVFAVAFVSKALH-TPNFLLSLALADMFGLVLP 90
 |||||
 DB 17 VEKVLLTFEFAMVIMAILGNLWVAVCRDRLKRTKTNFYISLAFADLVSVLVNAF 76
 |||||
 OY 91 STIRSVSCWFFGDFLCRLHTYLDLTLCLTSLIFHLCFSTIDRCAI-CDPLLYSKFT-V 148
 |||||
 DB 77 GAIELVDIMFEGMFLVRLTSLVLTFTASIFHLCCISLDRYAICQPLVYNNKMTPL 136
 |||||
 OY 149 RVALRYILAG-WGVPAATYSIFL-----YTDVETR-----LSQMLEMPCVG 190
 |||||
 DB 137 RIAL-MLGCGVPIPMFISFLPIMGWNNIGIVDIEKRKNHNSSTFCVFNKRPYAI 194
 |||||
 OY 191 SCQILLNKFWGMLNPFLEFVPCLMISLYKIFVAVATROAOQITTLKSLGAKAHER-- 248
 |||||
 DB 195 TCSVV-----AFYIPFLMLVLAHYRIYTAKEHAQIQMLQR--AGATSESRPQ 241
 |||||
 OY 249 -----KAKTGLIVGIYLLCWLPTIDMVDSLHFTTPPLVDFITWFA 294
 |||||
 DB 242 TADQSHTRMTETKAKATLCVINGCFCECAAPFVNIYDPFDIYPERKWTAFILMG 301
 |||||
 OY 295 YFNSACNPIIVFSGMFKKALTL 320
 |||||
 DB 302 YINGNLNPELYAFLNKSPRAFLIIL 327

RESULT 3

serotonin 4 receptor - rat
 S55549
 N:Alternate names: 5-HT receptor 4L
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Nov-1999
 C:Accession: S55549; S66494
 R:Gerald, C.; Adham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.;
 EMBO J. 14, 2806-2815, 1995
 A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization of
 A:Reference number: S55549; MUID:95317299; PMID:7796807
 A:Accession: S55549
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-406 <GER>
 A:Cross-references: GB:020907; NID:924640; PIDN:AAC52233.1; PID:924641
 R:Ulmer, C.; Schneck, K.; Kalkman, H.O.; Luebert, H.
 FEBS Lett. 370, 215-221, 1995
 A:Title: Expression of serotonin receptor mRNAs in blood vessels.
 A:Reference number: S66487; MUID:95385798; PMID:7656980
 A:Accession: S66494
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 95-259 <DLG>
 A:Cross-references: EMBL:248153; NID:984171; PIDN:CAA88170.1; PID:984172
 A:Experimental source: tissue brain
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 25.0%; Score 446.5; DB 2; Length 406;
 Best Local Similarity 33.1%, Pred. No. 3.6e-30;
 Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

OY 33 IQLVLYLT-CAAGMLIIVLGNVFAVAFVSKALH-TPNFLLSLALADMFGLVLP 90
 |||||
 DB 17 VEKVLLTFEFAMVIMAILGNLWVAVCRDRLKRTKTNFYISLAFADLVSVLVNAF 76
 |||||
 OY 91 STIRSVSCWFFGDFLCRLHTYLDLTLCLTSLIFHLCFSTIDRCAI-CDPLLYSKFT-V 148
 |||||
 DB 77 GAIELVDIMFEGMFLVRLTSLVLTFTASIFHLCCISLDRYAICQPLVYNNKMTPL 136
 |||||
 OY 149 RVALRYILAG-WGVPAATYSIFL-----YTDVETR-----LSQMLEMPCVG 190
 |||||
 DB 137 RIAL-MLGCGVPIPMFISFLPIMGWNNIGIVDIEKRKNHNSSTFCVFNKRPYAI 194
 |||||
 OY 191 SCQILLNKFWGMLNPFLEFVPCLMISLYKIFVAVATROAOQITTLKSLGAKAHER-- 248
 |||||
 DB 195 TCSVV-----AFYIPFLMLVLAHYRIYTAKEHAQIQMLQR--AGATSESRPQ 241
 |||||
 OY 249 -----KAKTGLIVGIYLLCWLPTIDMVDSLHFTTPPLVDFITWFA 294
 |||||
 DB 242 TADQSHTRMTETKAKATLCVINGCFCECAAPFVNIYDPFDIYPERKWTAFILMG 301
 |||||
 OY 295 YFNSACNPIIVFSGMFKKALTL 320
 |||||
 DB 302 YINGNLNPELYAFLNKSPRAFLIIL 327

RESULT 4

histamine H2 receptor - guinea pig
 J04120
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 24-Nov-1999
 C:Accession: J04120
 R:Triffort, E.; Vizuete, M.L.; Tardivel-Lacombe, J.; Souli, E.; Schwartz, J.C.; Ruat
 Biochem. Biophys. Res. Commun. 211, 570-577, 1995
 A:Title: The guinea pig histamine H2 receptor: gene cloning, tissue expression and ch
 A:Reference number: J04120; MUID:95314628; PMID:7794271
 A:Accession: J04120
 A:Molecule type: DNA
 A:Residues: 1-359 <TRA>
 C:Comment: Histamine, a messenger molecule in cell-to-cell communication, affects its
 ly defined receptor subtypes named H1, H2 and H3.
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F:22-45/Domain: transmembrane #status predicted <TM4>
 F:58-81/Domain: transmembrane #status predicted <TM4>
 F:93-113/Domain: transmembrane #status predicted <TM3>
 F:113-157/Domain: transmembrane #status predicted <TM4>
 F:157-204/Domain: transmembrane #status predicted <TM5>
 F:235-236/Domain: transmembrane #status predicted <TM6>
 F:269-289/Domain: transmembrane #status predicted <TM7>
 F:4162.168/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:4162.316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred
 F:226.357/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred

Query Match 23.5%; Score 420; DB 2; Length 359;
 Best Local Similarity 33.1%, Pred. No. 5.5e-28;
 Matches 103; Conservative 58; Mismatches 118; Indels 32; Gaps 10;

OY 21 NGSCPR-----TVHTGLIQLVLYLTCAAGMLIIVLGNVFAVAFVSKALHTPTNFIILS 75
 |||||
 DB 4 NGTVPSFCMDPTVYKVTISVILITL-----ILVTAGNVVAVGLAVLRRLRLSLNCFIVS 59
 |||||
 OY 76 LALADMFGLVLYLPLSTIRSVSCWFFGDFLCRLHTYLDLTLCLTSLIFHLCCISIDRCA 135

```

Db      60 LAATDILLGLVLPFSALITQLSCKWSKVFNCINILYSVLWMLCTASTLNFMSLDYCA 119
      136 ICDPLLYPSKFT-VRAVRLIAGMGVPAATSLFVETRLVETRLSOWLEEMPCVGSOL 194
      120 VDPPLRYVITPARAVALISVFI-WVI--SITLSFSLIIGWMSRNETSKDNDITVACKV 176
      195 LNKRFMGWLN-FPLFFVPCILMISLYKIFVATROAQITTLTSKSLAGAAKHEKRAKT 253
      177 QNVEYGLVDGLVTFVLPILMCIITYPRIKIAREQARI INHIG-SKKAATIREKKAFTV 235
      254 LGIVGVIYLLCMLP-FRI-----DTMDSLHFTTFLVNDIFITWPAFNSACNPII 304
      236 LAAVMGAFIICWPEYFVYRGLKGDADVAEVE-----DVLVLMIGYANSALNPIL 287
      305 YVFSYQWFKKA 315
      288 YALNDRDFRKA 298

```

RESULT 5

A40491
 alpha-1-adrenergic receptor - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A40491
 R:Cotechia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
 A>Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
 A:Reference number: A40491; MUID:89017157; PMID:2845338
 A:Accession: A40491
 A:Molecule type: mRNA
 A:Residues: 1-515 <COT>
 A:Cross-references: GB:J04084; NID:9619407; PID:AA51964.1; PID:9619408
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 23.5%; Score 419; DB 2; Length 515;
 Best Local Similarity 31.3%; Pred. No. 9.5e-28;
 Matches 110; Conservative 54; Mismatches 135; Indels 52; Gaps 8;

```

      21 NGSCPRTVHTLGIQVLYITLCAGMLITVGNFVAFAVYKRALHPTNFIQLSLALAD 80
      34 NSTLPQDITRAIS--VGLVGAFLIFAIIGNILVILSV:CNRLRTPPTVFIYNLMAAD 91
      81 MFTGLVLPSTIRSVSCWPFQDFLCRLHTYDITLFCILSIFHLCPISIDRHCAICDPL 140
      92 LLSTFYVLPFSATLEVLGIVWLGRIFCIDYAAADVLCCTISLSLCAISIDRTIGVXSL 151
      141 LYSKFTVRAALRYIAGMGVPAATSLFYTIDVETRLQMLEMPCVG-SCQLLNKF 199
      152 QYPLVYRRKAILALLSVW-----VLSTVISIPLGKMKRPANDKECGVTEPEF 202
      200 WG-WLNFPLFFVPCILMISLYKIFVATROAQI----- 233
      203 YALFSSIGSFYIPLAVILVMYCRVYIVAKRTKMLEAGVAKEMNSKELTLRIHSKNFHE 262
      234 TLTSLKSLAG-----AAK-----HERKAKTGIYVGIYLCWLPFTIDTWDSLHF 280
      263 DTLSSTAKGHNPRSSIAVLLFKFSREKKAATIGIYVGGFIICWLPFTIALPLGSLFST 322
      281 ITTP-LVFDIFITWPAFNSACNPIIYVFSYQWFKRALKTLISOKVFSPOTR 330
      323 LKPPDAVFKYVFMWLGYNFNSCLNPIIYPCSSKEFRARMLIGCGCRGRRR 373

```

RESULT 6

A45121
 alpha-1B adrenergic receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
 C:Accession: A45121; JG2332
 R:Ramirez, C.S.; Denker, J.M.; Perez, D.M.; Galvin, R.J.; Riek, R.P.; Graham, R.M.

J. Biol. Chem. 267, 21936-21945, 1992
 A>Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor
 A:Reference number: A45121; MUID:93016158; PMID:1328250
 A:Accession: A45121
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-517 <RAM>
 A:Cross-references: GB:M99590; NID:9178211
 A>Note: sequence extracted from NCBI backbone (NCBI:P116785)
 A>Note: this translation is not annotated in Genbank entry HUMADREN, release 113.0 #
 R:Wenborg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.
 Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
 A>Title: Cloning, expression and characterization of human alpha adrenergic receptors
 A:Reference number: JG2331; MUID:94296402; PMID:8024574
 A:Accession: JG2332
 A:Molecule type: mRNA
 A:Residues: 1-158, 'P', 160-244, 'H', 246-314, 'F', 316-380, 382-517 <HEI>
 C:Genetics:
 A:Gene: GDB:ADRA1B
 A:Cross-references: GDB:127901; OMIM:104220
 A:Map position: 5q31.1-5q33.2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:39-72/Domain: transmembrane #status predicted <TM1>
 F:81-111/Domain: transmembrane #status predicted <TM2>
 F:121-146/Domain: transmembrane #status predicted <TM3>
 F:157-184/Domain: transmembrane #status predicted <TM4>
 F:203-227/Domain: transmembrane #status predicted <TM5>
 F:290-320/Domain: transmembrane #status predicted <TM6>
 F:326-360/Domain: transmembrane #status predicted <TM7>

Query Match 23.4%; Score 418; DB 2; Length 517;
 Best Local Similarity 31.8%; Pred. No. 1.2e-27;
 Matches 107; Conservative 52; Mismatches 125; Indels 52; Gaps 8;

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      21 NGSCPRTVHTLGIQVLYITLCAGMLITVGNFVAFAVYKRALHPTNFIQLSLALAD 80
      34 NSTLPQDITRAIS--VGLVGAFLIFAIIGNILVILSV:CNRLRTPPTVFIYNLMAAD 91
      81 MFTGLVLPSTIRSVSCWPFQDFLCRLHTYDITLFCILSIFHLCPISIDRHCAICDPL 140
      92 LLSTFYVLPFSATLEVLGIVWLGRIFCIDYAAADVLCCTISLSLCAISIDRTIGVXSL 151
      141 LYSKFTVRAALRYIAGMGVPAATSLFYTIDVETRLSOWLEEMPCVG-SCQLLNKF 199
      152 QYPLVYRRKAILALLSVW-----VLSTVISIPLGKMKRPANDKECGVTEPEF 202
      200 WG-WLNFPLFFVPCILMISLYKIFVATROAQI----- 233
      203 YALFSSIGSFYIPLAVILVMYCRVYIVAKRTKMLEAGVAKEMNSKELTLRIHSKNFHE 262
      234 TLTSLKSLAG-----AAK-----HERKAKTGIYVGIYLCWLPFTIDTWDSLHF 280
      263 DTLSSTAKGHNPRSSIAVLLFKFSREKKAATIGIYVGGFIICWLPFTIALPLGSLFST 322
      281 ITTP-LVFDIFITWPAFNSACNPIIYVFSYQWFKKA 315
      323 LKPPDAVFKYVFMWLGYNFNSCLNPIIYPCSSKEFRARA 358

```

RESULT 7

A25896
 beta-adrenergic receptor - turkey
 C:Species: Meleagris gallopavo (common turkey)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 13-Aug-1999
 C:Accession: A25896
 R:Yarden, Y.; Rodriguez, H.; Wong, S.K.F.; Brandt, D.R.; May, D.C.; Bunniel, J.; Hark
 Proc. Natl. Acad. Sci. U.S.A. 83, 6795-6799, 1986
 A>Title: The avian beta-adrenergic receptor: primary structure and membrane topology.
 A:Reference number: A25896; MUID:86313664; PMID:3018746
 A:Accession: A25896
 A:Molecule type: mRNA
 A:Residues: 1-483 <YAR>

A:Molecule type: mRNA
A:Residues: 424-499 <HIR>
A:Cross-references: EMBL:D32202
C:Genetics:
A:Gene: GDB:ADRA1C; ADRA1L1
A:Cross-references: GDB:128088; OMIM:104221
A:Map position: 8p21-8p11.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 23.1%; Score 412.5; DB 2; Length 499;
Best Local Similarity 32.7%; Pred. No. 3.2e-27;
Matches 112; Conservative 51; Mismatches 126; Indels 53; Gaps 10;

QY 21 NSCPTVHTLGIQVLYLTCAGMLII-VLGNVFAVNSYKALHTPTNLLSLAL 78
DB 11 SSMCTOPAPAVNISKAIIIGVILGGLIFGVGLNIIILSVACHRHLSVTHYYINLAV 70
QY 79 ADMFLGLVLPSTISVSCFFGDFLCRLHTYLDTLF-LHSIFHLCTSIDRHCAICD 138
DB 71 ADLLLTSTVLPFSAIEVGLYMAFGVFCNMAAVDVLCTASIMGLCTISIDRYIGVSY 130
QY 139 PLIYPSKFTYRVLRITLAGMGVPAVTSFLTVDYET-ILSQMLEMPCVGS-CQLLN 197
DB 131 PLKPTIYTORGLMALCYW-----ALSLVIST-GPLFGMRQAPPEDETIQ--IN 179
QY 198 KFWGWLNFPL--FFVPCLMISLYKIEVATRO-----AQQTTL----- 236
DB 180 EEPGYLFSALGSFYLPAILIIMYCRVYVAKRESGL(SGLKTDKSDSEQYTLRIHRK 239
QY 237 -----SKSLAGAA-----KHKRAKTIGIV;IYLLCWLPTITDMVDSLH 279
DB 240 NAFAGSGGMAASAKTKTHFSYRLKFSREKRAKTLGIV;CFVLCWLPFLVMPIGSFFP 299
QY 280 FTRP-PLVPDIFIFWFAVNSACNPIIYVSYQWERKALK-TL 320
DB 300 DEKPSFTFRIVFWLGLNSCINPIIYPCSSQEFKRAFO;VL 341

RESULT 15

151661
dopamine D1C receptor - African clawed frog (fragment.
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #txxt_change 13-Aug-1999
C/Accession: 151661
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Nizn, K.; H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A>Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: 151659; MID:95024150; PMID:7337919
A:Accession: 151661
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:Cross-references: EMBL:U07865; MID:9559763; PIDN:AA50830.1; PID:9559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 23.0%; Score 411; DB 2; Length 465;
Best Local Similarity 32.3%; Pred. No. 4.1e-27;
Matches 106; Conservative 56; Mismatches 118; Indels 48; Gaps 11;

QY 31 LGIQVLYLTCAGMLIIVLGNVFAVNSYKALHTP-TNPLLSLALADMFLGLVLP 89
DB 25 LSLRALTLGLLSLILSTLIGNTLVCLAVIKFRHLSKVTNFEVLSLAVSDLFVALLVMP 84
QY 90 LSTIRVSCGFPGDFLCRLHTYLDTLFCLTSTIFHLCTSIDRHCAICDPLTPSKFTVR 149
DB 85 WKAVTEVAGFWVGDF-CDTWAFDIDMCSSTASILNLCISLDRYWALASPFRRERKWTQR 143
QY 150 VALRTIAGMGVPAVTSFLTVDYETRLSQWL-----EEMPCVGS--SCQLLNKFW 200
DB 144 VALIMIGVAM-----TSLISLTFIPVQLS-WKSHSEALEELNGVNHTECDSLNKTY 195

QY 201 GMLNFPL-FFVPCLMISLYKIEVATROAQOITTLK-----SLAGA 243
DB 196 AISSLSISFYIPVIMIGTYRTIYIAQTQIRRISSLERAVEHAQRCSSRLSNSLSKTS 255
QY 244 AKHKRAAKTLGIVGIIYLLCWLPTITDMVDSLHF-----TTPPLY-----EDIFTW 292
DB 256 FRKETVVLKTLSTIMGVFVFCWLPFVVLNCMIPFCHMNLPGQNEPBPVCVSETTFNIFW 315
QY 293 FAYNSACNPIIYVSYQWERKALKTL 320
DB 316 FGWANSLSNPVIYAFNAD-FKRAFITIL 342

Search completed: August 26, 2003, 14:25:23
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:21:42 ; Search time 13 Seconds

(without alignments)
1219.077 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785

Sequence: 1 MRAVPIQGAERHPAFCYQV.....LTLSQVPSPTRTVDLYOE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459.5	25.7	388	5H4_MOUSE	P97288 mus musculus
2	455.5	25.5	388	5H4_HUMAN	Q13639 homo sapien
3	452.5	25.0	388	5H4_CAVPO	O70528 cavia porce
4	446.5	25.0	406	5H4_RAT	O62758 rattus norv
5	432.5	24.2	466	5H4_MOUSE	P97718 mus musculus
6	432.5	24.2	466	5H4_RABIT	O02824 oryctolagus
7	422.5	23.7	379	5H4_FUGRU	P79748 fugu rubrip
8	420	23.5	359	5H4_CAVPO	P47747 cavia porce
9	419	23.5	515	5H4_MESAU	P18641 mesocricetu
10	418.5	23.4	466	5H4_CAVPO	O9w525 cavia porce
11	418	23.4	385	5H4_XENLA	O42574 xenopus lae
12	418	23.4	515	5H4_RAT	P15823 rattus norv
13	418	23.4	519	5H4_HUMAN	P35368 homo sapien
14	417	23.4	483	5H4_MOUSE	P07700 meleagris g
15	416.5	23.3	359	5H4_HUMAN	P25102 rattus norv
16	415.5	23.3	359	5H4_HUMAN	P25021 homo sapien
17	413.5	23.2	470	5H4_MOUSE	O91175 oryctolagus
18	412.5	23.1	466	5H4_HUMAN	P43140 homo sapien
19	412.5	23.1	466	5H4_RAT	P97922 mus musculus
20	411.5	23.0	465	5H4_MOUSE	P42291 xenopus lae
21	411	23.0	514	5H4_MOUSE	P97717 mus musculus
22	410.5	22.9	466	5H4_MOUSE	P18130 bos taurus
23	409.5	22.8	374	5H4_MOUSE	P28565 rattus norv
24	407.5	22.7	374	5H4_MOUSE	O61225 mus musculus
25	405	22.7	436	5H4_MOUSE	P31388 rattus norv
26	404.5	22.7	466	5H4_MOUSE	P34371 mus musculus
27	404.5	22.7	467	5H4_MOUSE	O9t596 bos taurus
28	404.5	22.7	467	5H4_MOUSE	O9t596 bos taurus
29	404	22.6	377	5H4_MOUSE	O288227 ovis aries
30	399.5	22.4	359	5H4_MOUSE	O288227 ovis aries
31	399.5	22.3	359	5H4_MOUSE	P17124 canis faml
32	398.5	22.3	363	5H4_MOUSE	P35406 carassius a
33	398.5	22.3	363	5H4_MOUSE	P35406 carassius a

34	397.5	22.3	459	1	D1DR_FUGRU	P53452 fugu rubrip
35	397.5	22.3	466	1	B1AR_RAT	P18090 rattus norv
36	397	22.2	440	1	5H6_HUMAN	P50406 homo sapien
37	396.5	22.2	377	1	5H1D_HUMAN	P28221 homo sapien
38	395.5	22.2	446	1	DADR_MACMU	O77680 macaca mula
39	395.5	22.2	474	1	B1AR_FELCA	O9t56 felis silve
40	394.5	22.1	428	1	B4AR_MELGA	P79148 canis faml
41	394	22.1	473	1	B1AR_CANFA	P43141 canis faml
42	393.5	22.0	446	1	DADR_HUMAN	P21728 homo sapien
43	393	22.0	377	1	5H1D_RABIT	P49145 oryctolagus
44	393	22.0	457	1	DBDR_XENLA	P42290 xenopus lae
45	392	22.0	451	1	DADR_XENLA	P42289 xenopus lae

ALIGNMENTS

RESULT 1
5H4_MOUSE STANDARD: PRT; 388 AA.
AC P97288; O89003; O89004; Q9R2A4;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5-hydroxytryptamine 4 receptor (5-HT-4) (Serootonin receptor) (5-HT4).
GN HTR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss; TISSUE=Brain;
MEDLINE=97102706; PubMed=8946946;
RA Claessen S., Sebben M., Journot L., Bockaert J., Dumuis A.;
RT "Cloning, expression and pharmacology of the mouse 5-HT(4l)
receptor.";
RL FEBS Lett. 398:19-25(1996).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Dumuis A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E)).
RX STRAIN=Swiss; TISSUE=Brain;
MEDLINE=99127199; PubMed=9928238;
RA Claessen S., Faye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;
RT "5-HT4 receptors: cloning and expression of new splice variants.";
RL Ann. N.Y. Acad. Sci. 861:49-56(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(F)).
RX TISSUE=Brain;
MEDLINE=9928795; PubMed=10220570;
RA Claessen S., Sebben M., Becamel C., Bockaert J., Dumuis A.;
RT "Novel brain-specific 5-HT4 receptor splice variants show marked
constitutive activity: role of the C-terminal intracellular domain.";
ML Pharmocol. 55:910-920(1999).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CYCLASE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-4;
Name-1;
IsoId=p97288-1; Sequence=Displayed;
Name=5-HT4(A);
IsoId=p97288-2; Sequence=VSP_001851;
Name=5-HT4(E);
IsoId=p97288-3; Sequence=VSP_001852;
Name=5-HT4(F);
IsoId=p97288-4; Sequence=VSP_001853;

FT	TRANSMEM	138	158		4 (POTENTIAL)
FT	DOMAIN	159	192		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	193	213		5 (POTENTIAL).
FT	DOMAIN	214	260		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	261	281		6 (POTENTIAL).
FT	DOMAIN	282	294		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315		7 (POTENTIAL).
FT	DOMAIN	316	388		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD		7		N-LINKED (GLCNAC...) (POTENTIAL).
FT	DISULFID	93	184		BY SIMILARITY.
FT	LIPID	329	329		PALMITATE (BY SIMILARITY).
FT	VASPLIC	169	169		L-> LERSLNQGGODFHFA (in isoform 5-HT4(E)).
FT					/FtId-VSP_001845.
FT	VASPLIC	359	388		RDAVCGGOWESQCCHPATSPPLVAAPSPT -> SGCSPVS
FT					SFLLEPCNRPPV (in isoform 5-HT4(E)).
FT	VASPLIC	359	388		/FtId-VSP_001846.
FT					RDAVCGGOWESQCCHPATSPPLVAAPSPT -> SSGTETD
FT	VASPLIC	360	388		RNRNGIRKRRRTKPS (in isoform 5-HT4(D)).
FT					/FtId-VSP_001847.
FT	VASPLIC	360	388		DVAVCGGOWESQCCHPATSPPLVAAPSPT -> F (in isoform 5-HT4(C)).
FT					/FtId-VSP_001848.
FT	VASPLIC	360	388		DVAVCGGOWESQCCHPATSPPLVAAPSPT -> YTVLARGH
FT					HQEELKLPINHDPESLSCF (in isoform 5-HT4(A)).
FT					/FtId-VSP_001849.
FT	VASPLIC	360	388		Missing (in isoform 5-HT4(G)).
FT					/FtId-VSP_001850.
SO	SEQUENCE	388 AA;	43761 MW;	7ECFBC60E7BD560 CRC64;	
	Query Match		25.5%;	Score 455.5; DB 1; Length 388;	
	Best Local Similarity		34.5%;	Pred. No. 7e-24;	
	Matches 110;	Conservative 59;	Mismatches 111;	Indels 39; Gaps 12;	
Oy	IQIIVLYIF-CAAGLLIIVGVNPAFANSYRKALH-TPTNFLLSLALADFLGLVLPL 90				
Db	17 VEVKVLLTFSTVTLLMLLGMLLVAAWCWROKRKTNTNFYSLSAPADLLVASLVMPF 76				
Oy	91 STINSVESCFEFDFCLRLMYLDLTFLCISIFHLCEFSIDRHOAI-CDPLLYSKFT-V 148				
Db	77 GAIELVODIMVIYGEEVFCFLVRSLDLVLTTSATPHLCISIDRYAAYICQPLVYNKKMPL 136				
Oy	149 RVALARITLAG-WGYPRAATSLFL-----YTIVVER-RLSQMLEBPCVGSQCOLLINK 198				
Db	137 RIAL--MLGGGWVPIPTSELPINQGNNGIIIDLIERKKNONSNSYCV----FYVNK 190				
Oy	199 FMG-WLNPPLFEVCLMISLYVAFVATQAQOITTLSSLSGAARKHER----- 248				
Db	191 PYAITCSVAVFYIFPLMLVLAIFYAKKAHQIQMLQR--AGASSESRPOSADQHS 248				
Oy	249 -----KAAKTGIAVGVIYLCLMLPEITDMVDLSLHFITTPPLVFDFIFAVENSACN 301				
Db	249 HRMRTEKAAKTTLCIIMGCCFCLCAAPFVTNIYVPFDIYVPGQWTAFLMWIGTNSGLN 308				
Oy	302 PIIVFVSQWRKAKLTLL 320				
Db	309 PELYAFLNKSERRAFLITL 327				
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RESULT 3					
ID	5H4_CAVPO	STANDARD:	PRT:	388 AA.	
AC	070528:				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	5-hydroxytryptamine 4 receptor (5-HT ₄) (Serotonin receptor) (5-HT ₄). HTR4.				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
NC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.				
OX	NCBI_Taxid=10141;				

FT	DOMAIN	123	143		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	144	167		4 (POTENTIAL).
FT	DOMAIN	168	181		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	182	205		5 (POTENTIAL).
FT	DOMAIN	206	273		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	274	297		6 (POTENTIAL).
FT	TRANSMEM	298	305		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	306	329		7 (POTENTIAL).
FT	DOMAIN	330	466		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	7	13		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	13	22		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	215	215		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	99	176		PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT	LIPID	345	345		BY SIMILARITY.
SO	SEQUENCE	466 AA;	51762 MW;	3649ASAS3DBD34DA CRC64;	
Query Match		24.2%	Score 432.5:	DB 1:	Length 466:
Best Local Similarity		34.2%	Pred. NO. 2.8e-22:		
Matches 120:		Conservative 50:	Mismatches 114:	Indels 67:	Gaps 122
QY	HPAFRCVQNGNSCPRTVHTLTGQLIYLITCAAGMLII-VLGNVFAVAEVSFKALHPT	69			
Db	HPRA-----QVN-----ISRAILLGVLLGLIIGVLGNILVLSVACHRIHLST	61			
QY	NELLISLADLMETGLLVLPSTRSVESCSFFGGDFCLRLHTYDTFLCLSIHFILCETS	129			
Db	HYYVNIIVLAADLLTSPVALPFESAIFELIGYNAFGVFENIMAWDYLCCTASIMGLCIIS	121			
QY	IDRHCAICDPLLYESKFEVRALARVLIANGCVPAVTSLELYTDVVERLRSLWTEMPCY	189			
Db	IDRIIGVSYPRPIYIQRGVRRLLCW-----ALSLSISI--GPLFGWRQAPED	172			
QY	GS-CQLLNKFEGMLNPEL---FEVPCLMISLYVKIFVAVTRQ-----AQ	231			
Db	ETICO--INERPGYVLFSGLSFYPLIILVMCRVVYVANKRESRGLSKGLTKDKOSE	230			
QY	QIT-----TLKSFLAGAKH-----EKRAKTGLIYGVIYLLCMUPFTI	270			
Db	QVTLRIRHKRNYPABSGSVSAKNKTHFSRVRLKFSREKRKAATLDIGVCFVLCMLPEFL	290			
QY	DTMYDSL-HFITPELVEDIWEFAFENSACNPFIYVSQWFRAKLKLT	320			
Db	VMPGSEFPNNKRPETVEKIYFWLGYLNSCINPIIYPPSSSQEFKAFOENVL	341			
RESULT 6					
A1AA_RABIT STANDARD: PRT; 466 AA.					
AC	A1AA_RABIT	002824;			
DC	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).				
GN	ADRA1A OR ADRA1C.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
RN	NCBI_TaxID=9986;				
RX	(1)				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=97324192; PubMed=9180361;				
RA	Miyamoto S., Taniguchi T., Suzuki F., Takita M., Kosaka N., Negoro E., Okada T., Kosaka H., Murata S., Nakamura S., Akagi Y., Oshita M., Watanabe Y., Muramatsu I.;				
RT	"Cloning, functional expression and tissue distribution of rabbit alpha1a-adrenoceptor."				
RL	Life Sci. 60:2069-2074(1997).				
CC	-I- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL- CALCIN SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(O) AND G(I1) PROTEINS.				

Query Match	Best Local Similarity	Score	DB 1:	Length	466:
Matches 114; Conservative 53; Mismatches 121; Indels 55; Gaps 10.					
QY 21	NGSCPRTVHTGLDLYITFCAGGLIT--VLGNVFAFAVSFKALHTPTNFLLSLAL 78				
Db 11	SSNCTHPAPAPNISKAILLVIGLLIGLVGLVGNILVLTLSVACHRHLSVTHYYIVNLAV 70				
QY 79	ADNMLGLLVPLSTIRSVESCMFQDPLCRHTHTYIDLTPCLSTPHLCFISIDRHCACID 138				
Db 71	ADLLTSTVTFEFSALFEILGYWARGVRCNIMWADVLCSTASISLVIDRITIGVSY 130				
QY 139	PLTPSKRTVVALRYITLWAGVDAALYSLFLYTDVET--RLSQWLEEMPCGS--COLLL 196				
Db 131	PLRPFTIYTORGRGLBALCVNA-----FSLVVISVGLFGRQAPDDETICQ--I 178				
QY 197	NKFWGMNFP--FEVPCLMISLYKIFVATRO-----AQQIT----- 234				
Db 179	NEERGVLVSLAGSFYVPLITIIAMCYVVVYAKRNSGKLSGKTKDRSDSEQVYTLRIHR 238				
QY 235	---TLSSLSLAGAAR-----ERAAKTLIGVGTILYLCWLPFTIIDWVDSL 278				
Db 239	KNABAGSGVSAANKKTHFSVRLKFSNREKRAKTLIGVLCFVLCWLPFLVMPDGSEFF 298				
QY 279	HFIRPP-LVFDIFLWFAFNACNPIIVFVSQYOMFRKALTKTL 320				
Db 299	PDFKPEPVEKIVFEMGLTNSCINPIIIPCSQSEKKAFOVNL 341				

SHID_FUGRU STANDARD: PRT: 379 AA.

ID SHID_FUGRU

AC P97748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 5-hydroxytryptamine 1D receptor (5-HT-1D) (Serotonin receptor) (5HT1D) (F11D).

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes; Tetraodonidae; Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Testis;

RX MEDLINE=97361762; PubMed=9218723;

RA Yamaguchi F., Brenner S.;

RT Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor gene from the Japanese puffer fish, Fugu rubripes.";

RL Gene 191:219-223(1997).

CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.

CC -----

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CC -----

DR EMBL: X83865; CAA58745.1; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1

DR PRINTS: PR00237; GPCRHOOPSN.

DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECPT_FL2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family.

FT DOMAIN 1 36

FT TRANSMEM 37 60

FT DOMAIN 61 73

FT TRANSMEM 74 96

FT DOMAIN 97 106

FT TRANSMEM 107 132

FT DOMAIN 133 152

FT TRANSMEM 153 174

FT DOMAIN 175 192

FT TRANSMEM 193 216

FT DOMAIN 217 307

FT TRANSMEM 308 331

FT TRANSMEM 332 339

FT TRANSMEM 340 364

FT TRANSMEM 365 379

FT DISULFID 109 186

FT CARBOHYD 5 5

FT CARBOHYD 14 14

FT CARBOHYD 21 21

FT SEQUENCE 379 AA: 42301 MM; 99862C0379EBC78 CRC64;

Query Match 23.7%; Score 422.5; DB 1 Length 379;

Best Local Similarity 30.8%; Pred. No. 1, 1e-21;

Matches 109; Conservative 60; Mismatches 108; Indels 77; Gaps 10;

OY 31 LGIQIVYITLCAAGMLIIVGNVAVAFVAFALHTPINFLLSLADMLGLVPL 90

DB 33 LGIQISVYLAIVTLATMLSNFVATIFLTRKHTPANFLIGSLAVDMVSLVMP 92

OY 91 STIRSVESCFEFDICRLHTYDITFLCFLSTFHLCISIDRICALCDPLLYSKRTVAV 150

DB 93 STYTVSKTWSLQIQICDILWSSDITFCASIIHLCLVIALDRWATDIALEYSKRTMR 152

OY 151 ALRYIILAGMGVPAAYSLFLYTDVETRLSOMLEMPVCVSCOLLN---KRWGLNLP 206

DB 153 AAMVAVVWYI-----SISMPPLWRQAKAHELK-----ECWNTQIDISTLYSTRG 202

OY 207 LEFVPLIMISLYVKIFVAFRQ-----AQOI-TTLKSL----- 240

DB 203 AFVYPTVLLIIIGRIYVAARSRIFTPSYSGKRTTAQLIQTSAGSSLSLSANSNOEA 262

OY 241 ---AGA-----AKHEKAKTGIYVGLICWLP 268

DB 263 HLHSGAGGEGGSPLEFVNSYKVLADNVLERKLCARERKAKRTIGIIGAFIICWLP 322

OY 269 TIDTWDLSLHFTT-PPLVEDIFIMFAYFNSACNPIITV-YES---YOMPKALK 317

DB 323 FVYTLVWALCKECSFDPDLFDVYTWGLYLSLNPVITYVFENDFQARQKLIK 376

RESULT 8

ID HH2R_CAVPO STANDARD: PRT: 359 AA.

AC P47747;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Histamine H2 receptor (H2R) (Gastric receptor 1).

GN HHR2.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC SPRAIN-Hartley; TISSUE-Liver;

RA Traifort E.;

RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U25440; AAA65713.1; -

DR PIR: JCA120; JCA120.

DR HSSP: P28274; 1MMH.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHOOPSN.

DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECPT_FL2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Domain 1 22

FT DOMAIN 1 22

FT TRANSMEM 23 44

FT TRANSMEM 45 57

FT TRANSMEM 58 81

FT DOMAIN 82 92

FT TRANSMEM 93 114

FT DOMAIN 115 134

FT TRANSMEM 135 159

4 (POTENTIAL).

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FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 181 204 5 (POTENTIAL).
FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 235 258 6 (POTENTIAL).
FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 268 289 7 (POTENTIAL).
FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).
FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).
FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 91 174 BY SIMILARITY.
SO SEQUENCE 359 AA; 40556 MW; 58DB1BD8FC3C0E9 CRC64;

Query Match 23.5%; Score 420; DB 1; Length 359;
Best Local Similarity 33.1%; Pred. No. 1.6e-21;
Matches 103; Conservative 58; Mismatches 118; Indels 32; Gaps 10;

OY 21 NGSCPR-----TVHTLGIQIVYITLCAAGMLIIVGNFVAVAFYKALHTPTNELLS 75
DB 4 NGIVPSCMDFYVKVITSVILIL-----ILVTVAGNVVCLAVGLNRLSLNCFIVS 59
OY 76 LALADMFGLVLPSTIRSVESCFGDFLCRLHYLDLFCLSIFHLCFISIDRCA 135
DB 60 LAVDLLGLVLPFSAIYOLSCKMSFSKVCNITSLDVALCTASILNLFMISIDRCA 119
OY 136 ICDLLPDKRT-VRAVLRYLAGWCPAATSLFLYTDVETRLSCWLEMPVGSQQL 194
DB 120 VTDLRFPVLITPARVAISLFTI-WVI--STLSFLSHLGMNSRNETSKNDITVCKV 176
OY 195 LANKFMGLN-FPLFEVPCILIMISLYKIEFVATROAQOITLSLGAKEHKAKT 253
DB 177 QVNEVYGLVDSLVFVPLMLCMCTYFRIFKAREQARINHG-SWMAATIRREKAVT 235
OY 254 LGIVVGYILCWF-FIT-----DTMDSLHFTPLPVEDIFWFAVNSACNFI 304
DB 236 LAAMVAGFIICWFIEFVYRGLKGDVAWEFE-----DVLMLGYANSALNPI 287
OY 305 YVFSYQWPKKA 315
DB 288 YALNRPFRFA 298

RESULT 9
ALAB_MESAU STANDARD; PRT; 515 AA.
ID ALAB_MESAU
AC P18841;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_Taxid=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9901157; PubMed=2845398;
RA Cotechia S., Schwinn D.A., Randall R.R., Lefkowitz R.J.,
RA Caron M.G., Kobilka B.K.;
RT "Molecular cloning and expression of the cDNA for the hamster alpha
RT 1-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7159-7163(1988).
RP MOTAGENESIS OF ALA-293.
RX MEDLINE=92112850; PubMed=1346134;
RA Kjelsberg M.A., Cotechia S., Ostrowski J., Caron M.G.,

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RA Lefkowitz R.J.;
RT "Constitutive activation of the alpha 1B-adrenergic receptor by all
RT amino acid substitutions at a single site. Evidence for a region
RT which constrains receptor activation.";
RL J. Biol. Chem. 267:1430-1433(1992).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; J04084; AAA58964.1; -.
DR PIR; A40491; A40491.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 46 70 1 (POTENTIAL).
FT DOMAIN 71 83 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 84 105 2 (POTENTIAL).
FT DOMAIN 106 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 141 3 (POTENTIAL).
FT DOMAIN 142 161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 201 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 202 224 5 (POTENTIAL).
FT DOMAIN 225 295 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 296 319 6 (POTENTIAL).
FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 327 340 7 (POTENTIAL).
FT DOMAIN 341 515 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 371 378 POLY-ARG.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 118 195 BY SIMILARITY.
FT LIPID 365 365 PALMITATE (POTENTIAL).
FT MUTAGEN A->X: CONFERS CONSTITUTIVE ACTIVITY.
SQ SEQUENCE 515 AA; 56492 MW; 6DAF1576D1CCE2D CRC64;

Query Match 23.5%; Score 419; DB 1; Length 515;
Best Local Similarity 31.3%; Pred. No. 2.4e-21;
Matches 110; Conservative 54; Mismatches 135; Indels 52; Gaps 8;

OY 21 NGSCPRVHTLGIQIVYITLCAAGMLIIVGNFVAVAFYKALHTPTNELLSLAD 80
DB 34 NSTPLQDLPRAIS-VGLVIGAFILRAIVGNILVSVACNRLRPTNFYINAIAD 91
OY 81 MFDGLVLPSTIRSVESCFGDFLCRLHYLDLFCLSIFHLCFISIDRCAICDPL 140
DB 92 LLLSEFVLPFSATLEVGLVIGRIFEDIMAAVDVLCCTASILSCAISIDRYIGVRS 151
OY 141 LYSKFTYRVALRKTIYLAGWCPAATSLFLYTDVETRLSCWLEMPVGSQQLLNKF 199
DB 152 QPPLVTRKATILALSLW-----VSTVISIGPLLGKWPAPNDKCEGTBEFP 202
OY 200 WG-MLNPLFVPCILIMISLYKIFVAVATROAQI----- 233
DB 203 YALFSSIGSFYIPLAVILVMTCRVYIAKRTTKNLGKWKEMSKNELRLIRSKNFHE 262

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OY 234 TTLSKSLAG-----AAK-----HERAAKTIGIVGIIYLLCWLPTIIDMVDLSLH 280
DB 263 DTLSTFKAGHNPRESSIAVLEKFSREKRAKTLGIVGCFILCWLPTIATLPLGSLFST 322
OY 281 IPPP-LVPDIFIMFAVENSACNPITYVFSYOMFRKALKLISQKVSPOQR 330
DB 323 LKPPDAVFNVMELGTFNSCLNPIIYPCSSKEFKAFMRILGQCRSGRR 373

RESULT 10
ALAA_CAVPO STANDARD: PRT: 466 AA.
AC 09W025;
DB 16-OCT-2001 (Rel. 40, Created)
DB 16-OCT-2001 (Rel. 40, Last sequence update)
DB 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-1a adrenergic receptor (Alpha 1a-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21419075; PubMed=11527538;
RA Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M.,
RA Gonzalez-Espinosa D., Garcia-Sainz J.A.;
RT "Molecular cloning and functional expression of the guinea pig
RT alpha(1a)-adrenoceptor."
RL Eur. J. Pharmacol. 426:147-155(2001).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC AND G(11) PROTEINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF108016; AAD23540.2; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Phosphorylation; Palmitate.
FT DOMAIN 1 25
FT TRANSMEM 26 51
FT DOMAIN 52 63
FT TRANSMEM 64 89
FT DOMAIN 90 99
FT TRANSMEM 100 122
FT DOMAIN 123 143
FT TRANSMEM 144 168
FT DOMAIN 169 181
FT TRANSMEM 182 205
FT DOMAIN 206 272
FT TRANSMEM 273 297
FT DOMAIN 298 304
FT TRANSMEM 305 329
FT DOMAIN 330 466
FT LIPID 345 345
FT CARBOHYD 13 13
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 466 AA; 51577 MW; E0E27EAF5D30DCD CRC64;
Query Match 23.4%; Score 418.5; DB 1; Length 466;
Best Local Similarity 32.5%; Pred. No 2.4e-71;
Matches 111; Conservative 54; Mismatches 124; Indels 53; Gaps 9;

OY 21 NGSCPTVHTLGIVLYITCAAGMLI--VLGNVFAVAVSKALHPPTNLISLAL 78
DB 11 SNNCTQPPAPAVNIPKAILLGVILGLVILFQVNPNIILVILSVACHRHLSHTHYIYNLAV 70
OY 79 ADMFGLIVLPSTISVESCFFGDFLCRLHLYLTLCISIFHLCFISIDRCAICD 138
DB 71 ADLLSTVLPFSAIEIILGVMAFGRVFCINMAVAVLCTASTIMSCITISIDRYGVSV 130
OY 139 PLIYPSKFWYRVAVLRTILAGWGPAAVTSVLTVDVETRLSQMLEMPVGS-COLLIN 197
DB 131 PLKFPYIVYQRLRLALICM-----ALSVIST--GFLFGWRQAPADETICO--IN 179
OY 198 KFWGMLNFPVLP--FVPCCLIMISLYVKIFVVAATRAQOITTLSSK----- 239
DB 180 EDRSVYLFSAIGSFYVPLAILIWMYCRVYVAVKRESGLTSGKTQSDSEQYTLRIHRK 239
OY 240 ---LAGAA-----KHEKAAKTIGIVGIIYLLCWLPTIIDMVDLSLH 279
DB 240 NAEPLGGSGVAASSKNKTHFSVRLKFSREKRAKTLGIVGCFILCWLPTIATLPLGSLFST 299
OY 280 FIVP-LVPDIFIMFAVENSACNPITYVFSYOMFRKALKLTL 320
DB 300 DFKPSETVRIYVWLGTLNSCLNPIIYPCSSSEFKAFQNVYL 341

RESULT 11
BLAR_XENIA STANDARD: PRT: 385 AA.
AC 042574;
DB 15-JUL-1998 (Rel. 36, Created)
DB 15-JUL-1998 (Rel. 36, Last sequence update)
DB 15-JUL-1998 (Rel. 36, Last annotation update)
DE Beta-1 adrenergic receptor (X-BETA1AR).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98055670; PubMed=9395292;
RA Devic E., Faquereau L., Kagnad M., Steinberg R., Caput D.,
RA Audigier Y.;
RT "Early expression of a beta1-adrenergic receptor and catecholamines
RT in xenopus oocytes and embryos.*"
RL FEBS Lett. 417:184-190(1997).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CARBOXYLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y09213; CAAT0415.1; -
DR HSSP: P07700; 1DEP.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1.1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECIP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multiligand family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 37
FT TRANSMEM 38 61
FT DOMAIN 62 71
FT TRANSMEM 72 88
FT DOMAIN 89 109
FT TRANSMEM 110 131
FT DOMAIN 132 153
FT TRANSMEM 154 174
FT DOMAIN 175 200
FT TRANSMEM 201 223
FT DOMAIN 224 272
FT TRANSMEM 273 297
FT DOMAIN 298 303
FT TRANSMEM 304 326
FT DOMAIN 327 385
FT CARBOHYD 12 12
FT DISULFID 108 187
FT LIPID 340 340
SO SEQUENCE 385 AA; 43309 MW; 0153D05AE49E0C1B CRC64;

Query Match      23.48; Score 418; DB 1; Length 385;
Beet Local Similarity 33.28; Pred. No. 2.2e-21;
Matches 109; Conservative 47; Mismatches 124; Indels 48; Gaps 9;

OY 25 PRTHV--TIGIQIYIYLTCAGMLIIVGNFVAFNAYFRKALHTPPFLLSLADMF 82
DB 28 PELTHQMTGNTM---NAIIILIVGNIMVYALGRNRLDTLTINVFITSLACADLI 83
OY 83 LGLVLPSTIRSVESCFEGDFLCRLTLYDTLFTCLTSIFLHCISIDRCATCDPLLY 142
DB 84 MGLFVPLIGATLVYSGRLVGSIFCEFTSYDVLCAVSIETLCVISIDRIATSPERY 143
OY 143 PSKFTVNALRYIIAGMCPVPAVYSLPYTDVETRLSQMLE-----MPCV---GSCQ 193
DB 144 QSLITKGRAGKIVSWGISLVSFLPT-----MMHWNRDYGDLAMKCYEDPGCD 195
OY 194 LLLKFMQMLNFPF--FEVPCLLIMISLVYKIFVATROAQI----- 233
DB 196 FVTNRVAVALASISIFEPFLIMFVYIRVFEKAKQKIDKCEGRSHSVLSHGSS 255
OY 234 -TTLSKSLAGAAKERRAAKTLGVIVGYLLCWLPTFTIDVADSLHETTPPLVDFITW 292
DB 256 RRIISKLIVY---KEOKALKTLGIIMGFTLCWLPFLANVNVFYRNLIPDKLFLFLNW 312
OY 293 FAYENSACNPITYFYSQWFRKALKTL 320
DB 313 LGVANSANPILTYCRSPD-FRKAKRRL 339

RESULT 12
ID ALAB_RAT STANDARD. PRT: 515 AA.
AC P15823; 063215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=90192094; PubMed=2156222;
RA Voigt M.M., Kispert J., Chin H.;
RT "Sequence of a rat brain cDNA encoding an alpha-1B adrenergic

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RT receptor.";
RL Nucleic Acids Res. 18:1053-1053(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91177889; PubMed=1706716;
RA Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A.,
RA Yang-Feng T.L., Brownstein M., Leikowitz R.J., Caron M.G.;
RT "Molecular cloning and expression of the cDNA for the alpha 1A-
RT adrenergic receptor. The gene for which is located on human
RL chromosome 5.";
RL J. Biol. Chem. 266:6365-6369(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010315; PubMed=8406017;
RA Gao B., Kinos G.;
RT "Isolation and characterization of the gene encoding the rat alpha 1B
RT adrenergic receptor.";
RL Gene 131:243-247(1993).
RN [4]
RP SEQUENCE OF 1-253 FROM N.A.
RX MEDLINE=95081407; PubMed=7989580;
RA Kanasaki M., Matsubara H., Murasawa S., Masaki H., Mio Y., Inada M.;
RT "cAMP responsive element-mediated regulation of the gene
RT transcription of the alpha 1B adrenergic receptor by thyrotropin.";
RL J. Clin. Invest. 94:2245-2254(1994).
CC -1 FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL; X51585; CAA35934.1; -
DR EMBL; M60655; AAA63478.1; -
DR EMBL; L08610; AAA40647.1; -
DR EMBL; L08609; AAA40647.1; JOINED.
DR EMBL; D32045; BAA06806.1; -
DR PIR; J01525; J01525.
DR HSSP; P29274; IMMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1.1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECIP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multiligand family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45
FT TRANSMEM 46 70
FT DOMAIN 71 83
FT TRANSMEM 84 105
FT DOMAIN 106 115
FT TRANSMEM 116 141
FT DOMAIN 142 161
FT TRANSMEM 162 182
FT DOMAIN 183 201
FT TRANSMEM 202 224
FT TRANSMEM 225 295
FT DOMAIN 296 319
FT TRANSMEM 320 326
FT DOMAIN 327 340
FT TRANSMEM 341 371
FT DOMAIN 371 378
FT CARBOHYD 10 10
FT CARBOHYD 24 24
FT DISULFID 34 34
FT DISULFID 118 195

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FT LIPID 365 365 PALMITATE (POTENTIAL).
FT CONFLICT 114 116 GRI -> LSF (IN REF. 2).
FT CONFLICT 203 203 Y -> C (IN REF. 1 AND 4).
FT CONFLICT 207 207 S -> C (IN REF. 1 AND 4).
FT CONFLICT 306 306 C -> S (IN REF. 3).
FT CONFLICT 415 416 HQ -> OK (IN REF. 1).
FT CONFLICT 440 440 C -> Y (IN REF. 3).
FT CONFLICT 484 486 GDT -> ATA (IN REF. 1).
FT CONFLICT 493 493 T -> S (IN REF. 3).
FT CONFLICT 511 511 A -> G (IN REF. 1).
SQ SEQUENCE 515 AA; 56585 MW; AF0C3759F80C3135 (RC64);

Query Match 23.4%; Score 418; DB 1; Length 515;
Best Local Similarity 31.8%; Pred. No. 2,8e-21;
Matches 107; Conservative 52; Mismatches 125; Indels 52; Gaps 8;

OY 21 NSCSPTVHTLGLQVLYITCAAGMLIYGNVFAVAYFRALHTPTNLLSLALND 80
DB 34 NSTLPLQDVYTRALS--VGLVLGAFLEFAIVGNLVLVYCNHLPPTNYFTVNLAD 91
OY 81 MFLGLVLPSTIRSVESQWFGDFLCRLHTYLDLFCULSIFHLCFISIDRCAICDPL 140
DB 92 LLSTFVLPFSATLEVLGVMVIGRIFCDIMANDVLCCTSLISLCAISIDRIGVRYSL 151
OY 141 LYSKFTVVALRYIAGVGPAAVYSLPYTDVETRL3QWLEEMPCVG-SCQLLNKF 199
DB 152 QPPTVTRRAKAILALISLV-----VLSTVVISIGPLGMRKAPANDKEGVMEEPF 202
OY 200 WG-WLNFPLEFVPCLMISLVYKIFVATROAOI----- 233
DB 203 YALFSSLSGFYPLAVILVMYCRVYVARTKTNLAGYKREMSNSKELTLRISHSNFHE 262
OY 234 TILSKSLAG-----AAK-----HERKAKTIGIVGILYLCWLPFTIDTWDSLHF 280
DB 263 DTLSSKAKGHNPRSSINAKLFESREKKAKTIGIVGAFILCWLPPFIALPLGSLFST 322
OY 281 TRPP-LVPDIFTFMAYFNSACNPIIVSYQMFRA 315
DB 323 LKPPDAVFYVFWLGTGFNSCLNPIIYPCSSKEFKRA 358

RESULT 13
ALIB_HUMAN STANDARD; PRT; 519 AA.
ID ALIB_HUMAN
AC P35368;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=93016158; PubMed=1328250;
RA Ramarao C.S., Denker J.M., Perez D.M., Galvin R.J., Risk R.P.,
RA Graham R.M.;
RT "Genomic organization and expression of the human alpha 1B-adrenergic
RT receptor."
RT J. Biol. Chem. 267:21936-21945(1992).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=94239386; PubMed=8183249;
RA Forray C., Baid J.A., Wetzel J.M., Chiu G., Shajiro E., Tang R.,
RA Lepor H., Hartig P.R., Weinschank R.L., Branchek T.A.,
RA Gluchowski C.;
RT "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RT the cloned human alpha 1c subtype."
RL Mol. Pharmacol. 45:703-708(1994).

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RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwaun D.A., Johnston G.I., Page S.O., Mosley M.J., Wallson K.H.,
RA Norman N.P., Campbell S., Fildock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues."
RL J. Pharmacol. Exp. Ther. 272:114-114(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M99589; -; NOT_ANNOTATED_CDS.
CC EMBL; M99590; -; NOT_ANNOTATED_CDS.
CC EMBL; U03865; AAB60352.1; -.
CC EMBL; L31773; AAB59485.1; -.
CC PIR; A45121; A45121.
CC HSSP; P28274; 1MMH.
CC DR Genew; HGNC; 278; ADRA1B.
CC DR MIM; 104220; -.
CC DR GO; GO:0005887; C: integral to plasma membrane; TAS.
CC DR GO; GO:0004937; F: alpha1-adrenergic receptor activity; TAS.
CC DR GO; GO:0008283; P: cell proliferation; TAS.
CC DR GO; GO:0007267; P: cell-cell signaling; TAS.
CC DR GO; GO:0007186; P: G-protein coupled receptor protein signaling. . .; TAS.
CC DR GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleo. . .; TAS.
CC DR GO; GO:0007243; P: protein kinase cascade; TAS.
CC DR Interpro; IPR000276; GPCR_Rhodopsn.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCR_RHODOPSN.
CC DR PROSITE; PS00237; G-PROTEIN_RECPT_F1.1; 1.
CC DR PROSITE; PS50262; G-PROTEIN_RECPT_F1.2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.
CC KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
CC FT DOMAIN 1 45
CC FT TRANSMEM 46 70
CC FT DOMAIN 71 83
CC FT TRANSMEM 84 105
CC FT DOMAIN 106 115
CC FT TRANSMEM 116 141
CC FT DOMAIN 142 161
CC FT TRANSMEM 162 182
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CC FT TRANSMEM 202 224
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CC FT TRANSMEM 296 319
CC FT DOMAIN 320 326
CC FT TRANSMEM 327 340
CC FT DOMAIN 341 519
CC FT DOMAIN 370 379
CC FT CARBOHYD 10 10
CC FT CARBOHYD 24 24
CC FT CARBOHYD 29 29
CC FT CARBOHYD 34 34
CC FT DISULFID 118 195
CC FT LIPID 365 365
CC FT CONFLICT 370 370
CC FT CONFLICT 379 379
CC FT CONFLICT 497 500
CC SQ SEQUENCE 519 AA; 56778 MW; C4727A147D0A1780 CRC64;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92028990; PubMed=1930188;
 RA Ruat M., Traillfort E., Arrang J.-M., Leurs R., Schwartz J.-C.;
 RT "Cloning and tissue expression of a rat histamine H2-receptor gene";
 RL Biochem. Biophys. Res. Commun. 179:1478-1478(1991).
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
 ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: S57565; AAB19935.1; -
 DR PIR: J01278; J01278.
 DR HSSP: P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 22
 FT TRANSMEM 23 44
 FT DOMAIN 45 57
 FT TRANSMEM 58 81
 FT DOMAIN 82 92
 FT TRANSMEM 93 114
 FT DOMAIN 115 134
 FT TRANSMEM 135 159
 FT DOMAIN 160 179
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 FT TRANSMEM 234 257
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 FT DISULFID 91 173
 FT SEQUENCE 358 AA; 40253 MW; 4889F69B7B5D5DDC CRC64;
 SQ
 Query Match 23.3%; Score 416.5; DB 1; Length 358;
 Best Local Similarity 31.8%; Pred. No. 2, 7e-21;
 Matches 106; Conservative 53; Mismatches 127; Indels 47; Gaps 9;
 QY 27 TVH-----TLGIQVLYITFCAGMLITVGNVFAFAV;YFKALHTPTNELLSLALAD 81
 DB 6 TVHSCGLDSMALKVTISVLTLLITLITINGNVVCLAV;LNRRLRSITNCFIYSLATDL 65
 QY 82 FIGLIVLPSTIRSVSCWFEFGDLRLRTITDYTLFCLISIFHLCTISIDRCACIDPDL 141
 DB 66 LIGLLVLPSPSAIYQISFTWSFGHVFNCIYTSIDVMLCT;SINLTFMISIDRYCAVDPDL 125
 QY 142 YPSKFT-VVVALRYILAGWGVPAAYSLFYTQVETRI;SOMLEMPCVG-----SCOLL 195
 DB 126 YFVLVTPVAVVAISLVFI-VWISTLSFLSHLG-----WNSRNGTRGNDTFCKQV 176

QY 196 LNFQWGLN-FPLEFVPCILIMISLYKIFVATROAQOITLTSKSLAGAAHRRKAATL 254
 DB 177 VNEVYGLVDSGLVTFEYLPILIMCTVYYRIEFILAREQAKRIWHIS-SMKAATIRHKATVTL 235
 QY 255 GIIVGYILQWLPF-----TIDTWDSLHFTYPPLVFDIFWFAVENSACN 301
 DB 236 AAVMGAFILICWPFYFAFYRGILRGDDALNEAVEG-----IVLMIGYANSALN 283
 QY 302 PIIVFSYQWFRKALTLTSQKVFSPQTRTVDL 334
 DB 284 PILYALNDRFRTAYOQLFHCKFASHNSHRTSL 316

Search completed: August 26, 2003, 14:24:11
 Job time : 15 secs

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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:22:07 : Search time: 40 Seconds
(without alignments)
2174.093 Million cell updates/sec

Title: US-09-988-745-2
Perfect score: 1785
Sequence: 1 KRAVFIQGAEEHPAFCYQV.....LTLSQKTESPQRTVDLYGE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1785	100.0	337	4	014804	014804 homo sapien
2	843.5	47.3	374	11	0923X9	0923X9 rattus norv
3	836.5	46.9	344	11	0923Y3	0923Y3 rattus norv
4	836.5	46.9	358	11	0923Y1	0923Y1 rattus norv
5	830.5	46.5	358	11	0923Y2	0923Y2 rattus norv
6	825.5	46.2	344	11	0923Y0	0923Y0 rattus norv
7	815.5	45.7	338	11	0923X8	0923X8 rattus norv
8	812.5	45.5	343	4	096R19	096R19 homo sapien
9	808.5	45.3	358	11	0923X6	0923X6 rattus norv
10	805	45.1	345	11	0923Y5	0923Y5 rattus norv
11	802.5	45.0	358	11	0923X5	0923X5 rattus norv
12	797.5	44.7	358	11	0923Y4	0923Y4 rattus norv
13	795.5	44.6	338	11	0923Y6	0923Y6 rattus norv
14	786.5	44.1	345	4	096R18	096R18 homo sapien
15	785.5	44.0	342	4	096R14	096R14 homo sapien
16	744.5	41.7	362	11	0923X7	0923X7 rattus norv

17	740	41.5	347	11	0923Y7	0923Y7 rattus norv
18	696.5	39.0	306	4	09P1P5	09P1P5 homo sapien
19	678.5	38.0	338	6	08H264	08H264 macaca mula
20	677.5	38.0	339	4	096R10	096R10 homo sapien
21	674.5	37.8	343	4	09P1P4	09P1P4 homo sapien
22	657	36.8	332	11	0923Y8	0923Y8 mus musculu
23	623.5	34.9	332	11	08VH05	08VH05 rattus norv
24	617.5	34.6	332	11	0923Y9	0923Y9 rattus norv
25	498	27.9	328	13	09YH18	09YH18 fugu rubrip
26	489.5	27.4	352	13	09YH14	09YH14 lampetra fi
27	489	27.4	328	13	09YH17	09YH17 fugu rubrip
28	484	27.1	353	13	09YH13	09YH13 lampetra fi
29	455.5	25.5	378	4	096KH9	096KH9 homo sapien
30	455.5	25.5	387	4	096KH0	096KH0 homo sapien
31	455.5	25.5	388	4	081KH9	081KH9 homo sapien
32	439.5	24.6	334	5	09NHF3	09NHF3 alypsia cal
33	435.5	24.4	508	5	09VC23	09VC23 drosophila
34	434.5	24.3	394	5	09NJS6	09NJS6 alypsia kur
35	432.5	24.2	425	6	09MZU2	09MZU2 oryctolagus
36	432.5	24.2	427	11	08BUE5	08BUE5 mus musculu
37	432.5	24.2	429	6	09MZU3	09MZU3 oryctolagus
38	432.5	24.2	466	11	08BV77	08BV77 mus musculu
39	424	23.8	518	6	09MY18	09MY18 oryctolagus
40	421.5	23.6	340	13	09YH12	09YH12 lampetra fi
41	418	23.4	459	11	08CG15	08CG15 mus musculu
42	418	23.4	515	11	09DB10	09DB10 mus musculu
43	414.5	23.2	466	4	096RE8	096RE8 homo sapien
44	413.5	23.2	358	11	09QX37	09QX37 mus musculu
45	413.5	23.2	397	11	09D282	09D282 mus musculu

ALIGNMENTS

RESULT 1
ID 014804
AC 014804; PRELIMINARY; PRT; 337 AA.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative neurotransmitter receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98125534; PubMed=9464258;
RA Zeng Z., Fan P., Rand E., Kyaw H., Su K., Madike V., Carter K.C.,
RA Li Y.;
RT "Cloning of a putative human neurotransmitter receptor expressed in
RT skeletal muscle and brain."
RL Biochem. Biophys. Res. Commun. 242:575-578(1998).
CC -1- SIMILARITY: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF021818; AAC39581.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001917; NHRtransf_2.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00599; AA_TRANSF_CLASS_2; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL2; 1.
DR PROSITE: PS00261; G_PROTEIN_RECPT_FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 337 AA; 38300 MW; 32134652B85CB35A CRC64;

Query Match 100.0%; Score 1785; DB 4; Length 337;
Best local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIGAEHPAFACFYQVNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVS 60
 DB 1 MRAVFIGAEHPAFACFYQVNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVS 60
 QY 61 YFKALHPPTNLLSLADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTPCLT 120
 DB 61 YFKALHPPTNLLSLADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTPCLT 120
 QY 121 SIFHLCFISIDRHCACDPLLPKFTVRALRYILAGWGPAAVTSLELYTDVETRLS 180
 DB 121 SIFHLCFISIDRHCACDPLLPKFTVRALRYILAGWGPAAVTSLELYTDVETRLS 180
 QY 181 QMLEEMPCVSCQILLKFKWGLNPLFEVPCLLMISLYKIVFAVATROAOQITTLSSSL 240
 DB 181 QMLEEMPCVSCQILLKFKWGLNPLFEVPCLLMISLYKIVFAVATROAOQITTLSSSL 240
 QY 241 AGAKHERKAKTIGIVGILLCMLEPPTIDTMDSLHFTTPPLVEDIFTFMFAVFNASC 300
 DB 241 AGAKHERKAKTIGIVGILLCMLEPPTIDTMDSLHFTTPPLVEDIFTFMFAVFNASC 300
 QY 301 NPIIVFSYQWFRKALKITLSQKVPSPOTRTVDLYOE 337
 DB 301 NPIIVFSYQWFRKALKITLSQKVPSPOTRTVDLYOE 337

RESULT 2

QY 0923X9 PRELIMINARY; PRT: 374 AA.
 AC 0923X9;
 DT 01-DEC-2001 (Tremblrel, 19, Created)
 DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
 DE Trace amine receptor 11.
 GN TAIL.
 OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC Mammalia; Eutheria;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowaky B., Adham N., Jones K.A., Raddatz R., Artyomshyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RT "Trace amines: identification of a family of mammalian G protein-
 coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF380199; AAK71250.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000585; Hemopexin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SO SEQUENCE 374 AA; 41495 MW; C88FDE2D04AA7AB CRC64;

Query Match 47.3%; Score 843.5; DB 11; Length 374;
 Best Local Similarity 45.8%; Pred. No. 6.7e-66;
 Matches 154; Conservative 68; Mismatches 103; Indels 11; Gaps 2;

QY 13 PAACFYQ-VNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVSFKALHTPTNF 71
 DB 39 PLQCYEVNVAASCKITPYSPGLRYLVLVWFGAVLAVCGMLLVIVSLHFKOLHSPANF 98
 QY 72 LLSLADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTPCLTSEFHLCEFTSID 131
 DB 99 LIALASADFLVGLVSPFMSVRSIESQWFGDFPCSLHSCDAFCYSLEFLCEFTSYD 158

QY 132 RHCAICDPLLPKFTVRALRYILAGWGPAAVTSLELYTDVETRLSQMLEEMPCVGS 191
 DB 159 RYIAVTDPLVPKFTVTSVSGICISIMILPLVYSSAVFTGATGIEMLVSLANCVGG 218
 QY 192 COLLKFKWGLNPLFEVPCLLMISLYKIVFAVATROAOQITTLSSSL 241
 DB 219 CQIVNDWVLIIDPLILPLVMIILSKFLVAKOAVKIEFTSISGSGESSLESKHA 278
 QY 242 GAHERKAKTIGIVGILLCMLEPPTIDTMDSLHFTTPPLVEDIFTFMFAVFNASC 301
 DB 279 RVAKHERKAKTIGIVGILLCMLEPPTIDTMDSLHFTTPPLVEDIFTFMFAVFNASC 338
 QY 302 PIIVFSYQWFRKALKITLSQKVPSPOTRTVDLYOE 337
 DB 339 PLIVAFEPWFRKALKITLSQKVPSPOTRTVDLYOE 374

RESULT 3

QY 0923Y3 PRELIMINARY; PRT: 344 AA.
 AC 0923Y3;
 DT 01-DEC-2001 (Tremblrel, 19, Created)
 DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
 DE Trace amine receptor 7.
 GN TAIL.
 OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC Mammalia; Eutheria;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowaky B., Adham N., Jones K.A., Raddatz R., Artyomshyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RT "Trace amines: identification of a family of mammalian G protein-
 coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF380195; AAK71246.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000585; Hemopexin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SO SEQUENCE 344 AA; 38043 MW; 45C41C861E5F6408 CRC64;

Query Match 46.9%; Score 836.5; DB 11; Length 344;
 Best Local Similarity 46.1%; Pred. No. 2.5e-65;
 Matches 153; Conservative 67; Mismatches 101; Indels 11; Gaps 2;

QY 17 CYQ-VNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVSFKALHTPTNF 75
 DB 13 CYENVNVAASCKITPYSPGLRYLVLVWFGAVLAVCGMLLVIVSLHFKOLHSPANF 72
 QY 76 LALDMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTPCLTSEFHLCEFTSIDRHC 135
 DB 73 LASADFLVGLVSPFMSVRSIESQWFGDFPCSLHSCDAFCYSLEFLCEFTSYDRIA 132
 QY 136 ICDDLPLLPKFTVRALRYILAGWGPAAVTSLELYTDVETRLSQMLEEMPCVSCQL 195
 DB 133 VTEPLVPKFTVTSVSGICISIMILPLVYSSAVFTGATGIEMLVSLANCVGGQVA 192
 QY 196 LNKFKWGLNPLFEVPCLLMISLYKIVFAVATROAOQITTLSSSL 245

ID	Accession	Protein Name	Score	DB	Length
Db	193	IN0DWN1SLFLPFIPLWMIILXSKFLVAKQAAVIEISIGSKESSESLSHKARVAK	252		
Qy	246	HERKAAKTGIVGIVYLLCMLPTTIDTMDVSLHFTTPTLVDFITFWEAFNSACNPIY	305		
Db	253	REKRAKTLGVTAFAVMSLPYITDPLIDAFMGFTIPAPVAYETICGMIAVYNSAMNPLIY	312		
Qy	306	VFESQWFRKALKTLFSOKVFSPPQRTVDLYOE	337		
Db	313	AFETPMFRKAKITLISGRILKGHSSITSLSE	344		

RESULT	Accession	Protein Name	Score	DB	Length
4	0923Y1	PRELIMINARY;	358 AA.		
AC	0923Y1				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
GN		Trace amine receptor 9.			
OS		Rattus norvegicus (Rat).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX		NCBI_taxid=10116;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RC		STRAIN=Sprague-Dawley;			
RX		MEDLINE=21374364; PubMed=11459929;			
RA		Botowsky B., Adham N., Jones K.A., Radatz R., Atyewshyn R.,			
RA		Ogozalek K.L., Durkin M.W., Lakhiani P.P., Bonini J.A., Pathirana S.,			
RA		Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,			
RA		Branchek T.A., Gerald C.;			
RT		"Trace amines: identification of a family of mammalian G protein-			
RT		coupled receptors."			
RL		Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).			
CC		-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC		-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR		EMBL: AF80197; AAK1248.1; -			
DR		InterPro: IPR000276; GPCR_Rhodpsn.			
DR		Pfam: PF00001; 7tm1.1; 1.			
DR		PRINTS: PR00237; GPCR_RHODOPSIN.			
DR		PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR		PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW		G-protein coupled receptor; Receptor; Transmembrane.			
SO		SEQUENCE 358 AA; 39962 MW; 0B392B5C312A8A3 JRC64;			

Query Match	Score	DB	Length
Best Local Similarity	45.5%;	Pred. No. 2,6e65;	
Matches 150;	Conservative 70;	Mismatches 101;	Indels 9; Gaps 2

ID	Accession	Protein Name	Score	DB	Length
Qy	17	CY0-VNGSCPTVHTLGIDLVYLLCAAGMLIYGVNFAVAAYSEFKALHPTNFWLLS	75		
Db	29	CYENINRSCVRSPPSPGSRLLIYAVFGFGLAVAGCNLLVMTSLHRLHSPANFLVLS	88		
Qy	76	LALADWFTGLVLPSTIRSVESCFEGDGLRCLRTYTLDFLCNISFIHCFISIDRGA	135		
Db	89	LACADILVGLTVPESMVAHSVCEGCTFGISYCKHSCFISICSSSLHLCISVDNRHA	148		
Qy	136	ICDDPLLPSEFTVRAALRYILAGWGPAAVTSLEFITYDVEFRLSOMLEEMPCVSCQL	195		
Db	149	VSDPLIYPRFTASVSGKITYFTSMLSIIYGFSLITGASEAGLEDVLSALTCVGCQYA	208		
Qy	196	LNKFGWMLPFLFEVCLIMISLYVIVFAVPAQAOQITLSKSLAGA-----AKHE	247		
Db	209	VNSQWFIPLFLFVLAALVMAVYSKIFELAKQAOAMHMKSQTPRAADSYKDRAKKE	268		
Qy	248	RKAAKTLGIVGIVYLLCMLPFTIDTMDVSLHFTTPTLVDFITFWEAFNSACNPIYV	307		
Db	269	RKAAKTLGIVGIVYLLCMLPFTIDTMDVSLHFTTPTLVDFITFWEAFNSACNPIYV	328		
Qy	308	SYQWFRKALKTLFSOKVFSPPQRTVDLYOE	337		
Db	329	EYEMFRKALKTLFSOKVFSPPQRTVDLYOE	358		

RESULT	5
Q923Y2	PRELIMINARY; PRT; 358 AA.
ID	Q923Y2
AC	Q923Y2
DT	01-DEC-2001 (TREMBLrel, 19, Created)
DT	01-DEC-2001 (TREMBLrel, 19, Last sequence update)
DT	01-MAR-2003 (TREMBLrel, 23, Last annotation update)
DE	Trace amine receptor 8.
GN	Ta8.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-Sprague-Dawley;
EX	MEDLINE=21374364; PubMed=11459929;
RA	Borowsky B., Adam N., Jones K.A., Radatz R., Artyushyn R.,
RA	Ogozalek K.L., Durkin M.M., Iakhlani P.P., Bonini J.A., Pathirana S.,
RA	Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA	Branchek T.A., Gerald C.;
RT	"Trace amines: identification of a family of mammalian G protein-
RT	coupled receptors."
RL	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; AF380196; AAK71247.1; -
DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm.1; 1.
DR	PRINTS; PR00237; GPCRHHODOPS.
DR	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR	PROSITE; PS50262; G_PROTEIN_REC_P1.2; 1.
KW	G-protein coupled receptor; Receptor; Transmembrane.
SEQ	SEQUENCE 358 AA; 40146 MW; E136ADA32C1A268B CRC64;
Query Match	46.5%; Score 830.5; DB 11; Length 358;
Best Local Similarity	45.8%; Pred. No. 8,8e-65;
Matches 151; Conservative	68; Mismatches 102; Indels 9; Gaps 2
QY	17 CQY-VNGSCPRTVATGIDLVYITLCAAGMLIYGVNFAVAFYKALHTPTNELLIS 75
DB	29 CYENLNGSCIRSPYSGPRLIIAYVFGGAVLAVCGNLIYVTSILHFRQLHSPANFLVAS 88
QY	76 IALAMFGLVLVLPSTIRSVSGCFEFGDFLCRLHTYIDTLQCLISIFHLCSIDRCA 135
DB	89 LACAPFLVGLVLPSTIRSVSGCFEFGDFLCRLHTYIDTLQCLISIFHLCSIDRCA 148
QY	136 ICDPLLYPSKFTVRALRYILAGWGPAYVLSLTFTYDVETRLSQWLEMPCVSGL 195
DB	149 VEDPLIYPRFRASVSGKCTFSMLSTIYSLSLYTGANENAGLDELVALTCVGCOLA 208
QY	196 LKFWGMLNPLFFPCLIMISLYKIFVAVARQAOITLTKSLAGA-----AKHE 247
DB	209 VNQSWVFIFLFLVPTLVMTVYISKIFLIAQQAQNMKSKQTTTASESYKDYAKRE 268
QY	248 RRAAKTIGLVGVGYLLCMLPFTIDFWDSLHFTPEPLVFDIFIFWAFYNSACNPLIYF 307
DB	269 RRAAKTIGLVGVGYLLCMLPFTIDFWDSLHFTPEPLVFDIFIFWAFYNSACNPLIYF 328
QY	308 SYQWFKALTKLTSQKVFSPQRTVDLYOE 337
DB	329 FYWPFKAIKILVTGKILRONSSVTMLPFE 358
RESULT	6
Q923Y0	PRELIMINARY; PRT; 344 AA.
ID	Q923Y0
AC	Q923Y0
DT	01-DEC-2001 (TREMBLrel, 19, Created)
DT	01-DEC-2001 (TREMBLrel, 19, Last sequence update)
DT	01-MAR-2003 (TREMBLrel, 23, Last annotation update)

DE Trace amine receptor 10.
 GN TAI0.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RT "Trace amines: Identification of a family of mammalian G protein-
 RT coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF380198; AAK71249.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 344 AA; 38015 MW; 6AB7A5CE3BE8692 CRC64;
 Query Match 46.2%; Score 825.5; DB 11; Length 344;
 Best Local Similarity 45.8%; Pred. No. 2,3e-64;
 Matches 152; Conservative 65; Mismatches 104; Indels 11; Gaps 2;
 OY 17 CYQ-VNGSCPRTVHTLGIQVLYTLCAAGMLIYGVNFAVAFVSKALHTPTNLLLS 75
 DB 13 CYENNAASIKTPYSPGLKLVLYVFGVAVCGNLVYISVLHFKQLSPANFLIAS 72
 OY 76 LALADMFLGLVLPSTIRSVESCFWFGDFLCRLHTYLDLFCGLTSIFHLCSIDRCA 135
 DB 73 LASADFLVGLVSPMSVRSIESCWYFQDFCSLHSCCDVAFCSALHLCPISDRITA 132
 OY 136 ICDPLVPSKFTVRAKLYIAGCVPAATYSLFTVDVETRLSOMLEMPCVGSCQL 195
 DB 133 VTDPLVPTKFTVSIGSICISWTLPLVSSAVFYGTISAMGIENLVSAIIVGCGQYV 192
 OY 196 LNKFWGMLNPLFEVPCIMISLYKIFVAVTRAOQITL-----LSKLAGAAK 245
 DB 193 VNQDMVLSLFLFTPLVMIILSKITLVAKQAIVLETISVSGSGSSLESKARVAK 252
 OY 246 HERAAKTLGIIVGILYLCWLPFTIDVWDSLHFTTPPLVDFIIFAVFNSACNPLIY 305
 DB 253 RERNAKTLGVTVLAFIVSWLPYITDILDAFMGFITPAVYERCCMSAVYNSAMNPLIY 312
 OY 306 VFSYOMFRKALTLTSOKVFSQPTRTVDLYOE 337
 DB 313 AFYFPMFRKAKLLISKILKGHSSTISLSE 344
 RESULT 7
 O923X8 PRELIMINARY; PRT; 333 AA.
 AC O923X8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Trace amine receptor 12.
 GN TAI2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RT "Trace amines: Identification of a family of mammalian G protein-
 RT coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF380200; AAK71251.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 333 AA; 37467 MW; 65BD86131C1C85B CRC64;
 Query Match 45.7%; Score 815.5; DB 11; Length 333;
 Best Local Similarity 44.8%; Pred. No. 1.7e-63;
 Matches 148; Conservative 67; Mismatches 106; Indels 9; Gaps 2;
 OY 17 CYQ-VNGSCPRTVHTLGIQVLYTLCAAGMLIYGVNFAVAFVSKALHTPTNLLLS 75
 DB 4 CYELNNSCVASPSPPRILLYVFGFVAVCGNLVMTSLHFKQLSPANFLVAS 63
 OY 76 LALADMFLGLVLPSTIRSVESCFWFGDFLCRLHTYLDLFCGLTSIFHLCSIDRCA 135
 DB 64 LACADFVGLVLPMSVRSIESCWYFQDFCSLHSCCDVAFCSALHLCPISDRITA 123
 OY 136 ICDPLVPSKFTVRAKLYIAGCVPAATYSLFTVDVETRLSOMLEMPCVGSCQL 195
 DB 124 VSDPLVPTKFTVSIGSICISWTLPLVSSAVFYGTISAMGIENLVSAIIVGCGQIA 183
 OY 196 LNKFWGMLNPLFEVPCIMISLYKIFVAVTRAOQITL-----AKHE 247
 DB 184 VNQSWVFNPLFLVPAVMTVYSKFLIAKQAQNIEMKGQTRABESYKDRARKE 243
 OY 248 RKAATLGIIVGILYLCWLPFTIDVWDSLHFTTPPLVDFIIFAVFNSACNPLIYF 307
 DB 244 RKAATLGIIVAAFLISWLPYITDILDAFMGFITPAVYERCCMSAVYNSAMNPLIY 303
 OY 308 SYOMFRKALTLTSOKVFSQPTRTVDLYOE 337
 DB 304 FYFPMFRKAKLIVTGKILRENSSATNLPPE 333
 RESULT 8
 O96R19 PRELIMINARY; PRT; 348 AA.
 AC O96R19;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Trace amine receptor 3.
 GN TA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RT "Trace amines: Identification of a family of mammalian G protein-
 RT coupled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL: AF380169; AAK71240.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRRHODOPS.
DR PROSITE: PS00237; G_PROTEIN_REEP_FL1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane
SEQUENCE 348 AA; 39016 MW; DDC64484880A6761 CcC64;

Query Match 45.5%; Score 812.5; DB 4; Length 348;
Best Local Similarity 46.1%; Pred. No. 3,2e-63;
Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3

```
OY CYO-VNGSCPTVPHLGIQIVLYLCAAGMLIIVGNFVNAVSYFRALHPPTFLLS 75
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db CYKAVNEECITTPSPGRSLIRAYLVGGAVALGAAFLNLIYAIIHFQOLHPPTFLIAS 73

OY 76 LALADMFGLLLPLSTIRSVESCSFCFDLCRLHTTYDTJECFLTSIFHLCEISIDRHA 135
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 74 LACADFVLGVVMPEPSIVRSVCWYFGDSCKFKTCDGTICCPASLFILCISIDRYIA 133

OY 136 ICDDPLVYSKRKTVPNALXYILLAGMVGVPAAVYSLEFYTDVVTRLSOMLEMPCVSQQL 195
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 134 VTFDPLTPFTKFTVSYGICVLAMFEFSVTYSFIETGANIEGIELVALTCVGGCCAP 193

OY 196 LNKEFMGLNFPLFEVPCILIMISLYKIFVVAATROAQOI-T'LSKSLAGA-----AKHE 247
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 194 LNQMNVLLCLFLFIPVANVAFYISKIFLPAVKHQARKIESASQAOSSESKERYAKE 253

OY 248 RKAKTIGIVGVYLCLMPTPTIDMDVSLHFTFPPLVEPIEIFAVAFNSACNPITYE 307
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 254 RKAKTTGIIAAGAEVSMPLPALVAIVDAVMFITPPVYVILIWCYYNSAMNDLIYAF 313

OY 308 SYQMFRRALKLTLSOKVPSPOTRPVLDLOE 337
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 314 FYQWFGRKRIKLIVSGKYLRTPSSITTNLFE 343
```

RESULT 9
Q923X6 PRELIMINARY; PRT: 358 AA.

AC Q923X6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Trace amine receptor 14.
GN TA14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrati; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowoky B., Adham N., Jones K.A., Raddatz R., Artymszyn R.,
RA Ogazalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtlan H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF380202; AAK71253.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRRHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 358 AA; 40216 MW; 516414ED0EFDF00 CcC64;

Query Match	Similarity	45.3%	Score 808.5	DB 11	Length 358
Best Local	Similarity	44.5%	Pred. No. 7.5e-63		
Matches 147	Conservative	69	Mismatches 105	Indels 9	Gaps 2
QY	17	QYQ-VNGSCPTVHTLGIQIQLVYLITLCAAGMLITVLGNFVAVAFVSKALHTPTNELL	75		
DB	29	CYENLNRSICSPSYSGPRLIHANVGFSAVLACGNLLVMYSILHFRQHSAPNFVA	88		
QY	76	LALADMFGLVLPLSTIRSVESCFEGDFLCRLHTFYDITLFTLSIFHLCTSIDRCA	135		
DB	89	LACADLLGLVLMPEFSVMRSVEGCVYFDIDYCKHFHSFSDVSCYSISFIHLCTSIDRYIA	148		
QY	136	ICDPLLYSKFTFVRALRYITLACVQVPAAYTSLFTYDIVERLRSQWLEEMCVSCOLL	195		
DB	149	VSDPLIYLFRRTASVSGKCIPTFSWPLSLIITSLSLYTCASEAGLEDVIALTCVGCOLA	208		
QY	196	LNRKEMGLNPLFEPVPCILMISLYKIFIVAVATROAQITTLTKSLAGA-----ARHE	247		
DB	209	VNOSVWFENFLFLFPLTVMYTSKVELIAKQAKNIEKIGKQPARASESKDRVAKRE	268		
QY	248	RRAKATIGVIGVILCWLPLFIDPMVDSLHFTIPPLVEDIFEMAFVNSGNTIYF	307		
DB	269	RRAKATIGITVAAFLPLSMPLPFIIDISIIILFAGFITPYVELVIAIYNSAMNLIYAF	328		
QY	308	SYQFRKALKLTLSQKFSPTQRTVDLYOE 337			
DB	329	FYPWFRKAIKILVTGKILRENSAVNLPE 358			
RESULT 10					
ID	Q923Y5	PRELIMINARY;	PRT;	345 AA.	
AC	Q923Y5;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
GN	T44.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN=Sprague-Dawley;				
RX	MEDLINE=21374364; PubMed=11459929;				
RA	Borowsky B., Adham N., Jones K.A., Raddatz R., Arcymyshyn R.,				
RA	Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,				
RA	Boyle N., Pu X., Konrathova E., Lichtblau H., Ochoa F.Y.,				
RA	Branchek T.A., Gerald C.,				
RT	"Trace amines: identification of a family of mammalian G protein-				
RT	coupled receptors."				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL: AF380191; AAK1242.1; -				
DR	InterPro: IPR000276; GPCR_Rhodopsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PRINTS: PR00237; GPCR_RHODOPSN.				
DR	PROSITE: PS50237; G_PROTEIN_RECPT_F1_1; 1.				
DR	PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.				
KW	G-protein coupled receptor; Receptor; Transmembrane.				
SO	SEQUENCE 345 AA; 38311 MW; DC90412705B406EC CRC64;				
Query Match	45.1%	Score 805;	DB 11;	Length 345;	
Best Local Similarity	43.9%	Pred. No. 1.5e-62;			
Matches 150;	Conservative 74;	Mismatches 106;	Indels 12;	Gaps 3;	
QY	8	GAEERPA---FCVQ-VNGSCPRTVHTLGIQIQLVITLCAAGMLITVLGNVAVAFVSK 63			
DB	2	GSNSPRAVLQCLTENNGSCVTKPIYSGRPVLLKAVFGFVALVATGNTLVMISILHFK 61			

```

QY 64 ALHPTNELLISLADMLGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIF 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 QLSHPTNELLISLACAPFWMGVSMFMSVRSIESCWFGFGRFCTPHCCVACVCSLF 121
QY 124 HLCSTIDRHCATDPLLYSKFTVVALRYILAGWGPAAVTSLEYTDVETRLSOML 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 HLSTISIDRYLAVNDPLVYPTKFTSVSGICISISMWILPLAYSGAVFTGTGADGLEBS 181
QY 184 EEMCVGSCOLLKFKFQMLNPLFPVPCILIMISLYKIFVAVATROAOITTLKSL--- 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 182 DAVACVGGCVVAVNNWNLIDFLSLFPLTLMILLYGIFLVAQOAKKIETVGNKAKSS 241
QY 241 ----AGAAKHEKRAKTLGIVGIIYLLCMLPFTIDVDSLHFTTPPLVDFIIFWY 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 242 SESYKARVARRERAKAKTLGITVAVAFMISMLPYSIDSLVDAFMGFTFPAYIYECWCA 301
QY 296 FNSACNPIIYFVSQWFRKAKLTLKSVKVSFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 302 YNSAMNPLIYALFYPMFKAKIKVMSQVFNSSATMNLFSSE 343

```

RESULT 11

```

Q923X5 PRELIMINARY; PRT; 358 AA.
AC 0923X5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Trace amine receptor 15.
GN TA15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF380203; AAK71254.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40652 MW; EEB84D9219EE1171 CRC64;

```

Query Match 45.0%; Score 802.5; DB 11; Length 358;
 Best Local Similarity 44.8%; Pred. No. 2.5e-62;
 Matches 148; Conservative 67; Mismatches 106; Indels 9; Gaps 2;

```

QY 17 CYQ-VNGSCPRTVHTLGIVLYLTCAAGMLIYLVGNFVAVAFYKALHPTNELLIS 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CYENINRSCVSPSPGRLILYAVFGGAVLAVCGNLMVMTSLHFRQLHSPANFLVAS 88
QY 76 LALADMLGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIFHLCEISIDRCA 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 LACADLVGLVMPSPVSMVRSVSGCWYFGDYCKLHCTCDVSCVSLHLCFISYDRIA 148
QY 136 ICDPLLYSKFTVVALRYILAGWGPAAVTSLEYTDVETRLSOMLEEMPCVSCQL 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 149 VSDPLIYIRRTASVSGKICITFSWMLSTIYGPPILYTGASBAGLKDVLSCVGCQIP 208
QY 196 LKMFQGMNPLFPVPCILIMISLYKIFVAVATROAOITTLKSLAGAA-----KHE 247

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```

DB 209 MNQKFLVINFLEFLVPLVMATVYSKIFLLRQAOQIEKKRKQFARASSESKDRVCKRE 268
QY 248 RKAATGIVGIIYLLCMLPFTIDVDSLHFTTPPLVDFIIFWAFNPSACNPIIYF 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 269 RKAATGIVAAVALLMLPFDISIDAFEGFTTPYVEILTIWYNSAMNPLIYAF 328
QY 308 SYQWFRKAKLTLKSVKVSFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 FYPMFRKAKIKVMSQVFNSSATMNLFSSE 358

```

RESULT 12

```

Q923Y4 PRELIMINARY; PRT; 358 AA.
AC 0923Y4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Trace amine receptor 6.
GN TA6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF380194; AAK71245.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40074 MW; CAE028CF9943DCE CRC64;

```

Query Match 44.7%; Score 797.5; DB 11; Length 358;
 Best Local Similarity 44.2%; Pred. No. 6.8e-62;
 Matches 146; Conservative 67; Mismatches 108; Indels 9; Gaps 2;

```

QY 17 CYQ-VNGSCPRTVHTLGIVLYLTCAAGMLIYLVGNFVAVAFYKALHPTNELLIS 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CYENINRSCVSPSPGRLILYAVFGGAVLAVCGNLMVMTSLHFRQLHSPANFLVAS 88
QY 76 LALADMLGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIFHLCEISIDRCA 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 LACADLVGLVMPSPVSMVRSVSGCWYFGDYCKLHCTCDVSCVSLHLCFISYDRIA 148
QY 136 ICDPLLYSKFTVVALRYILAGWGPAAVTSLEYTDVETRLSOMLEEMPCVSCQL 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 149 VSDPLIYIRRTASVSGKICITFSWMLSTIYGPPILYTGASBAGLKDVLSCVGCQIP 208
QY 196 LKMFQGMNPLFPVPCILIMISLYKIFVAVATROAOITTLKSLAGAA-----AKHE 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 MNQKFLVINFLEFLVPLVMATVYSKIFLLRQAOQIEKKRKQFARASSESKDRVCKRE 268
QY 248 RKAATGIVGIIYLLCMLPFTIDVDSLHFTTPPLVDFIIFWAFNPSACNPIIYF 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 269 RKAATGIVAAVALLMLPFDISIDAFEGFTTPYVEILTIWYNSAMNPLIYAF 328
QY 308 SYQWFRKAKLTLKSVKVSFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 FYPMFRKAKIKVMSQVFNSSATMNLFSSE 358

```

Query Match	44.68;	Score 795.5;	DB 11;	Length 338;
Best Local Similarity	45.58;	Pred. No. 9.7e-62;		
Matches 150;	Conservative 64;	Mismatches 107;	Indels 9;	Caps 3

[illegible]

Query Match	44.18;	Score 786.5;	DB 4;	Length 345;	.
Best Local Similarity	44.28;	Pred. No. 6.1e-61;			
Matches 146;	Conservative 70;	Mismatches 105;	Indels 9;	Gaps 3	

QY 17 CY -GVNGSCRYHTGIDLVLYLTCAGMLIYGVNFVAFAVSLHTPPNPLLS 75
 14 CYNVNGSCCKIPFSGSRVILLYIVGRCALVAFGNLLMISILHFKQLSPNPLVAS 73
 QY 76 LALADFLGLVLPLSTIRSVSCFEGEDLCRLHTYLDLFTCLTSIFLCLFISIDRCA 135
 74 LAADLVGVTVAFESMVRVTSACWYFGSFCFTFHCDVAFCSYLHCLFISIDRYIA 133
 QY 136 ICDPLLYPSKRYTRVALRYILAGMCPVPAAYTSLFYTVOVETRIQSOMEEMPCVGSQLL 195
 134 VTDPILYVPKRYFVSAGICISVWMLPLMYSANVYIVGVYDDGLELSDALNCGGCQY 193
 QY 196 LNFQWMLNPFLEFVPCMLINISLYKIRIVATROAOI--TLTSS-----LAGAKHE 247
 194 VNQNMVLTDFLSEFIPFTIMILYGNIFLVAHQKKILENGSKTESSESRYKARVARE 253
 QY 248 RKAATLGIIVGCIYLICWLPFTIDMNVDSLHFIETPPLFIDIFEMFAFENSACPRIYVE 307
 254 RKAATLGIIVAVAFMISMLPYSIDLIDAFNGEIRIPAIYVICCMCAVYNSAMNPLIYAL 313
 QY 308 SYQMPKALKLTLISQVSPQRYVDLYOE 337
 Db 314 FYPMERKALKVLYTGOVLNNSATINLSE 343

RESULT 15		
0969N4		
ID	0969N4	PRELIMINARY;
AC	0969N4	PRT; 342 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	G protein-coupled receptor (Trace amline receptor 5).	
GN	GPR102 OR TA5.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eultheria; Primates; Catarrhini; Hominoidea; Homo.	
OX	[1] NCBI_Taxid=9606;	
RN		
RP	SEQUENCE FROM N.A.	
RP	MEDLINE-21458557; PubMed-11574155;	
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhltko O.,	

RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT *Discovery and mapping of ten novel G protein-coupled receptors

genes: ";
Gene 275:83-91(2001).

[2]

RP SEQUENCE FROM N.A.
BY MONTYNE-31374364

SEQUENCE FROM N.A.
NUMBER-01274364

RX MEDLINE=213/4384; PubMed=11439929;

BA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathi

RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,

RA Brānchek T.A., Gerald C.;

RT "Trace amines: Identification of a family of mammalian G protein-

RT coupled receptors.";

Proc. Natl. Acad. Sci. U.S.A.
1961, 46:111-116.

DR EMBL; AF411118; AALZ048/.1; -
DB EMBL: AF380193; AAK71244.1; -

DB: Genew: HGNC:149664: GPR102.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PSS0464; G_PROTEIN_RECEP_F1_2; 1.

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NM      RECEIPT:
SQ      SEQUENCE: 342 AA: 38028 MW: AB034E6BF7D60388 CRC64:

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[illegible]

Query Match 44.08; Score 785.5; DB 4; Length 342;

Best Local Similarity 43.98; Pred. NO. 7.4e-61;

Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;

17 CWA-UNSCODRWIUMSTOYVITVETCAACMTITVTCNEIUAFAVSCVERATHEBTEIETIS 75

1 / C I Q - V N G S C F R I V H I D I Y V I I E I C A G M L I V G N V F V A F K V S I E N K H I F I N E L U S /

Db 13 CYEDVNGSCIETPYSPGSRVILYTAFSFGSLAVFNGNLLVMTSVLHFKOLHSPTNELIAS 72

76 LALADMEGLVLPSTIRSVESCMFEGDFLCRLHTYLDTLFCLTSIFHLCFISIDRHCA 13

[illegible]

Db 73 LACADELVGVTVMLFSMVRIVESCMYFGAKFCTLHSCCDVAFCYSSVLHLCFICIDRYIV 13

001 136 TCDOT VBSCWETPDIAT BVIT ACWCVBAVST ET VTNVWETPI SOWT FEMBCVSCOT. 19

130 1C D F L L I F S N E I V N V A H U N I I L W O M O V F H N I I D E F I I D V E I A N D O X U N D E E M F C V O D C U N N 1

Db 133 VTDPLVYATKFTVSVSVCISVSWILPLTYSGAVFYTGVNDGDGLEELVSALNCVGGCQII 15

QY 196 LNKFWGWLNEPFEVPCCLIMISLYVKIFVVATROAQITTLKSLAGA-----AKHE 24

Search completed: August 26, 2003, 14:24:57
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2003, 14:23:57 ; Search time 20 Seconds
(without alignments)
712.938 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
Sequence: 1 MRAVFIOGAHEHPAAFCYQV.....LTLSPVFSPTRTVDLYOE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/BACKFILE1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	337	2	US-08-467-559B-2
2	812.5	45.5	338	3	US-09-286-805-2
3	795.5	44.6	338	3	US-09-286-805-4
4	674.5	37.8	343	2	US-08-788-539A-2
5	455.5	25.5	360	4	US-09-555-113B-4
6	455.5	25.5	380	4	US-09-555-113B-24
7	455.5	25.5	388	4	US-08-446-822-8
8	455.5	25.5	388	4	US-09-328-314-8
9	455.5	25.5	388	4	PCT-US93-12586-8
10	455.5	25.5	760	4	US-09-555-113B-2
11	446.5	25.0	387	1	US-07-996-772A-2
12	446.5	25.0	387	1	US-08-446-822-2
13	446.5	25.0	387	5	US-09-328-314-2
14	446.5	25.0	387	5	PCT-US93-12586-2
15	446.5	25.0	406	4	US-09-328-314-4
16	444.5	24.9	406	1	US-07-996-772A-4
17	444.5	24.9	406	1	US-08-446-822-4
18	444.5	24.9	406	5	PCT-US93-12586-4
19	420	23.5	359	2	US-08-748-485-5
20	419	23.5	513	2	US-08-406-855A-21
21	419	23.5	513	3	US-09-206-899-21
22	419	23.5	515	1	US-08-444-734A-7
23	419	23.5	515	2	US-08-406-855A-22
24	419	23.5	515	3	US-09-206-899-22
25	419	23.5	515	4	US-09-688-415-9
26	419	23.5	515	4	US-09-688-415-10
27	418	23.4	515	1	US-08-722-001-25

28	418	23.4	517	2	US-08-467-568-10	Sequence 10, Appl
29	418	23.4	517	2	US-09-030-582-10	Sequence 10, Appl
30	418	23.4	520	1	US-08-334-698-4	Sequence 4, Appl
31	418	23.4	520	1	US-08-228-932-4	Sequence 4, Appl
32	418	23.4	520	1	US-08-468-939-4	Sequence 4, Appl
33	418	23.4	520	2	US-08-406-855A-4	Sequence 4, Appl
34	418	23.4	520	2	US-08-722-190-4	Sequence 4, Appl
35	418	23.4	520	3	US-08-244-354-4	Sequence 4, Appl
36	418	23.4	520	3	US-09-206-899-4	Sequence 4, Appl
37	418	23.4	520	4	US-09-444-783-4	Sequence 4, Appl
38	418	23.4	520	4	US-09-688-415-4	Sequence 4, Appl
39	418	23.4	520	5	PCT-US95-04203-4	Sequence 4, Appl
40	416.5	23.3	358	2	US-08-748-485-6	Sequence 6, Appl
41	416	23.3	515	3	US-09-032-742-5	Sequence 5, Appl
42	415.5	23.3	359	2	US-08-467-568-13	Sequence 13, Appl
43	415.5	23.3	359	2	US-08-748-485-4	Sequence 4, Appl
44	415.5	23.3	359	2	US-08-103-170-2	Sequence 2, Appl
45	415.5	23.3	359	2	US-09-030-582-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-08-467-559B-2
: Sequence 2, Application US/08467559B
: Patent No. 5928890
: GENERAL INFORMATION:
: APPLICATION: LI, YI
: TITLE OF INVENTION: HUMAN AMINE RECEPTOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/467,559B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: STEFFE, ERIC K
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488, 0840000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 337 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-467-559B-2

Query Match      100.0%; Score 1785; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-143;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAVFIOGAHEHPAAFCYQVNGSCPRTVHTIGIQLVYITLCAAGMLIIVGNFVAFAVS 60
        |||||||
DB      1 MRAVFIOGAHEHPAAFCYQVNGSCPRTVHTIGIQLVYITLCAAGMLIIVGNFVAFAVS 60
        |||||||

QY      61 YFAALHTPTNFFLLSLALADMPFGLVLPSTIRSVESCFPDGFLCRHTFYIDPLFCLT 120
        |||||||
DB      61 YFAALHTPTNFFLLSLALADMPFGLVLPSTIRSVESCFPDGFLCRHTFYIDPLFCLT 120
        |||||||
```

Qy	121	SIFHCFISIDBHCACIDPLKPSKFEYVAVALRYIAGAGVPAARYSLFYTYDVEBRUS	180
Db	121	SIFHCFISIDBHCACIDPLKPSKFEYVAVALRYIAGAGVPAARYSLFYTYDVEBRUS	180
Qy	181	QMLEBPCVGSQCLLLNFKFMGLNPLFVPCLLIMISLKVKIFVVVATROAQITTLTSSKL	240
Db	181	QMLEBPCVGSQCLLLNFKFMGLNPLFVPCLLIMISLKVKIFVVATROAQITTLTSSKL	240
Qy	241	AGAAHHERKAAKTLCIIVGCIYLLCWLPTITDMVDSLHFTTPPLVEDIFIMFAYNSAC	300
Db	241	AGAAHHERKAAKTLCIIVGCIYLLCWLPTITDMVDSLHFTTPPLVEDIFIMFAYNSAC	300
Qy	301	NPITIVFSYQWFRKALKTLSQKVSPORTYDLYOE	337
Db	301	NPITIVFSYQWFRKALKTLSQKVSPORTYDLYOE	337

RESULT 2
US-09-286-805-2
; Sequence 2, Application US/09286805

```

: PATENT NO. 611/990
: GENERAL INFORMATION:
: APPLICANT: Bonini, James A.
: APPLICANT: Borowsky, Beth E.
: TITLE OF INVENTION: DNA Encoding Orphan SMOF1 Receptor
: FILE REFERENCE: 58967
: CURRENT APPLICATION NUMBER: US/09/286,805
: CURRENT FILING DATE: 1999-04-06
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO 2
: LENGTH: 348
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-286-805-2

```

Query Match	45.5%	Score 812.5	DB 3	Length 348
Best Local Similarity	46.1%	Pred. No. 2.8e-61		
Matches 152; Conservative	64;	Mismatches 105;	Indels 9;	Gaps 3

[illegible]

RESULT 3
US-09-286-805-4
; Sequence 4, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Boninli, James A.
; APPLICANT: Borowsky, Beth E.

```

: TITLE OF INVENTION: DNA Encoding orphan Smor1 Receptor
: FILE REFERENCE: 58967
: CURRENT APPLICATION NUMBER: US/09/286,805
: CURRENT FILING DATE: 1999-04-06
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO 4
: LENGTH: 338
: TYPE: PRT
: ORGANISM: Rattus norvegicus
: US-09-286-805-4

```

ORGANISM: Rattus norvegicus
US-09-286-805-4

Query Match	44.68;	Score 795.5;	DB 3;	Length 338;
Post Local Classification	45.68;	Score 795.5;	DB 3;	Length 338;

Matches 150; Conservative 64; Mismatches 107; Indels 9; Gaps 3;

QY	17	CYO-VANGSCPRVHTIGIDLTLYILCAAGMLIIVGANEFAVSEFALHTPPNELL	75
		11 : 1111 : : : : : 11 : 11 : 11 : 11 : 11111111 : 11	
Db	4	CYENVNGSCIKSSYSWMPRAILIXAVIGALLAVNGNLVITTAHLHROLHTPTNEFLAS	63
QY	76	LALADNFGLLVLPSTINSVSCWFEFGDFLCRLHTTYIDTLFCLTSIFPHCETISIDRHC	135
		11 : 11 : 11 : 1111 : 1111 : 1111 : 1111 : 1111 : 1111 : 1111 : 1111	
Db	64	LACADPLVGYTAVPEFSTVSVSGCWYFSGJTYCKFPTCDTSEFCASLFIHLCCISIDRYVA	1233
QY	136	ICDPLLYPSKFYRVVALRYILAGWGPAAVYTSLEFYTVVETRTLSOMLEEMPCVSGCOLL	195
		1111 : 1111 : 1111 : 1111 : 1111 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11	
Db	124	VTDPPLRYTPRKTITSVSGVOCIALSWPFSVATYSRISFYTGANEDEGLVELVVALTYCQGGQAP	1633
QY	196	LKRFMGMLNPFLEFVYCLMISLYAKIPFVATROAQOTT-1LKSLSGA-----AKHE	247
		1111 : 11 : 1111 : : : : : 1111 : 11 : 1111 : : : : : 11 : 11 : 11 : 11	
Db	184	LONNMWLLCLFELEFPTVAVWVFLGYRIFLVAQAQRKLEGGANPQASSSEYKERVARR	2433
QY	248	RKAKTIGIYVGIYLLCWLPEFIDTMWSSLLFIHPIPLVEDFIWFAVENSACNPIYVE	307
		11111111 : : : 111 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11	
Db	244	RKAKTIGIIMAFIVSMPLPIIDAVDYNMFIIPAVYEELVWCYVYNSAMNPLIYAF	3030
QY	308	STOMFRKALKLTLSQKVFSPQRTYVDLQVE	337
		11111111 : 11 : 1111 : : : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11	
Db	304	FYPMFRKALKLVSGKVFADSSRTTLESE	333

RESULT 4
US-08-788-539A-2
; Sequence 2, Application US/08788539A

; FALENC NO. 38/198/
; GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: CLONING OF A NOVEL G-PROTEIN

TITLE OF INVENTION: COUPLED 7TM RECEPTOR
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: SMILNKline Beec
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA

COUNTRY: USA
 770 10405

```

;      20400
;      COMPUTER READAB

```

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; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible

```

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;
; OPERATING SYSTEM: DOS
SOFTWARE: FastSD for Windows Version 2.0
;

```

CURRENT APPLICATION DATA:
 ADDICTION NUMBER: ITS 608 4788 5302

FILING DATE: 24-JAN-1997

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: AIG5004/

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-788-539A-2

Query Match 37.8%; Score 674.5; DB 2; Length 343;
Best Local Similarity 39.4%; Pred. No. 1.3e-49;
Matches 130; Conservative 65; Mismatches 120; Indels 15; Gaps 3;

QY 23 SCPRVHTGIGLVITCAAGMLT-----IYGNVFAVAVSYFKALHTPTNELL 74
DB 12 SCPRFVNKLITSHQPLFSCPDNFGYDMSHDYPLRGMLYIMVISHFQLHSPNELL 71
QY 75 SLALADMFGLVLPSTIRSVSCWFGDELCLRLHTYLTLFELCSIFHLCSIDRHC 134
DB 72 SNAITDFLLGFYIMPIRISVSCWFGDGFCKHTSTFIMLRITSIHLCSTADRY 131
QY 135 AICDPLLYPSKFTVVALRYIILAGVCPAAYTSLFYTDVETRISQMLEMPCVSCOL 194
DB 132 ACYPLHYTKMTNSTIKQLARCVSPALFSGVLSELDVSGMQSVKILVACFMFCAL 191
QY 195 LNKFMGMANF-PLFVPCILIMSLVYKIFVATROAOQ:ITLKSLAGAA-----KHE 247
DB 192 TENKFGTLFTTCFTPGSINVGIGKIFVSKOHARV:SHNPETKGAVKKHLSKKD 251
QY 248 RKAATLGIVGIGVILCMLEPTIDTWDSLHFTPLPLVDIPMFAYFNSACNPIIYV 307
DB 252 RRAKTLGIVMGVFLACMLPCFLAVLIDPFLDYSTPLI:DLVWLRYFNSTGNPLIHG 311
QY 308 STOMERKALKLTLISQRFVSPQRTVDLYOE 337
DB 312 FNFMEFKAFKIVYSGKIFSSHSETANLPE 341

RESULT 5
US-09-555-313B-4
Sequence 4, Application US/09555313B
Patent No. 6506580
GENERAL INFORMATION:
APPLICANT: FICSHMEISTER, Rudolph et al.
TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
FILE REFERENCE: P067620500/BAS
CURRENT APPLICATION NUMBER: US/09/555,313B
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: FR 97/15037
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-555-313B-4

Query Match 25.5%; Score 455.5; DB 4; Length 360;
Best Local Similarity 34.5%; Pred. No. 4.4e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPNELLSLALADMFGLVLP 90
DB 17 VERKVVLLFTPLSTVIILAILGNLVMVAVCMDROLRIK:NYFLVSLAFADLVSVLMPF 76
QY 91 STIRSVSCWFGDFLCRLHTYDITLFCULSTIFHLCSIDRCAI-CDPLLYPSKFT-V 148

DB 77 GALEIVODIWIYGEVFCLVRTSLDVLITLTAISIFHLCCISLDRYYAICOPLYVRNMTPL 136
QY 149 RVALRYIILAG-WGVPAAYTSLFL-----YTDVETR-LSQMLEMPCVSCOLLNR 198
DB 137 RIAL-MLGCGWVIFPFISFLPIMOGMNNIGIIDLIEKKRFNONSSTYCV----PMVK 190
QY 199 FMG-WINPFLFVPCILIMISLVYKIFVATROAOQITTLTSLKSLAGAKHER----- 248
DB 191 PVAITCSVAAYFIPFLIMLAYRYIVTAKENHQIOMLOR--AGASSSRQSDAQHST 248
QY 249 -----KAKTLGIVGIGVILCMLEPTIDTWDSLHFTPLPLVDIPMFAYFNSACN 301
DB 249 HRRTETFKAKTLCIIMGCGFCICMAPEFVTNIVDPIDYVPGQVMTAFELMIGYINSGLN 308
QY 302 PIIVYSYOMFRKALKTL 320
DB 309 PFLYAFLNKSFRAFLITL 327

RESULT 6
US-09-555-313B-24
Sequence 24, Application US/09555313B
Patent No. 6506580
GENERAL INFORMATION:
APPLICANT: FICSHMEISTER, Rudolph et al.
TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
FILE REFERENCE: P067620500/BAS
CURRENT APPLICATION NUMBER: US/09/555,313B
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: FR 97/15037
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 380
TYPE: PRT
ORGANISM: Homo sapiens
US-09-555-313B-24

Query Match 25.5%; Score 455.5; DB 4; Length 380;
Best Local Similarity 34.5%; Pred. No. 4.6e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPNELLSLALADMFGLVLP 90
DB 17 VERKVVLLFTPLSTVIILAILGNLVMVAVCMDROLRIK:NYFLVSLAFADLVSVLMPF 76
QY 91 STIRSVSCWFGDFLCRLHTYDITLFCULSTIFHLCSIDRCAI-CDPLLYPSKFT-V 148
DB 77 GALEIVODIWIYGEVFCLVRTSLDVLITLTAISIFHLCCISLDRYYAICOPLYVRNMTPL 136
QY 149 RVALRYIILAG-WGVPAAYTSLFL-----YTDVETR-LSQMLEMPCVSCOLLNR 198
DB 137 RIAL-MLGCGWVIFPFISFLPIMOGMNNIGIIDLIEKKRFNONSSTYCV----PMVK 190
QY 199 FMG-WINPFLFVPCILIMISLVYKIFVATROAOQITTLTSLKSLAGAKHER----- 248
DB 191 PVAITCSVAAYFIPFLIMLAYRYIVTAKENHQIOMLOR--AGASSSRQSDAQHST 248
QY 249 -----KAKTLGIVGIGVILCMLEPTIDTWDSLHFTPLPLVDIPMFAYFNSACN 301
DB 249 HRRTETFKAKTLCIIMGCGFCICMAPEFVTNIVDPIDYVPGQVMTAFELMIGYINSGLN 308
QY 302 PIIVYSYOMFRKALKTL 320
DB 309 PFLYAFLNKSFRAFLITL 327

RESULT 7
US-08-446-822-8
Sequence 8, Application US/08446822
Patent No. 5766879

```
;; GENERAL INFORMATION:
;; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
;; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: COOPER & DUNHAM
;; STREET: 30 ROCKEFELLER PLAZA
;; CITY: NEW YORK
;; STATE: NEW YORK
;; ZIP: 10112
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,822
;; FILING DATE: June 1, 1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, P., John
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPM/NAT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 388 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-446-822-8

Query Match      25.5%; Score 455.5; DB 1; Length 388;
Best Local Similarity 34.5%; Pred. No. 4.7e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLIIVLGNVFAVAVSYFKALH-TPTNPLLSLALADWFLGLVLP 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 17 VEKVLLFTLSTVILMALIGNLVMAVACMDROLKIKTNFYISLAFADLLVSLVMPF 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 STIRSVESCMFEGDFCLRLHTYLDLPTLSIFHLCTSIDRHCAI-CDPLLYPSKFT-V 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 GATLVODIWIYGEVFCVRSLSVLTLTASIFHLCCISIDRYAALICQPLVYRNKMTPL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 RVALRYILIAG-WGVPAAVTSFL-----YTDVETR-LSQWLEMPCYGSCOLLNKL 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 RIAL--MGGCQWVLPFTISFLPIMGWNNIGIILIERKNQNSSTYCV----FWYVK 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 FWG-WLNEPFLFVPCLLIMISLYKIEFVATROAOITTLSSLAGAKHER----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 PYATCSVAAYIFPLMLVLAIRIYVAKHAHQIQMLQR--AGASESPQSDQHS 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -----KAATLGIIVGIIYLLCWLPTIDTMVDSLHFTTPPLVDFITFAVNSACN 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 HRMRTETAAKTLCTIIMCCFCLCWAPEFVNTIVDPFDITVPGQWTAFLMLGYINSGLN 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 PIIVFSYQWFRKALKLTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 PFLYAFLNKSFRRAPLITL 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-328-314-8
; Sequence 8, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschenk, Richard L.
```

```
;; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
;; FILE REFERENCE: 42667-A2-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/328,314
;; CURRENT FILING DATE: 1998-04-03
;; EARLIER APPLICATION NUMBER: 08/446,822
;; EARLIER FILING DATE: 1995-07-31
;; EARLIER APPLICATION NUMBER: PCT/US93/12586
;; EARLIER FILING DATE: 1993-12-22
;; EARLIER APPLICATION NUMBER: 07/996,772
;; EARLIER FILING DATE: 1992-12-24
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 388
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-328-314-8

Query Match      25.5%; Score 455.5; DB 4; Length 388;
Best Local Similarity 34.5%; Pred. No. 4.7e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLIIVLGNVFAVAVSYFKALH-TPTNPLLSLALADWFLGLVLP 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 17 VEKVLLFTLSTVILMALIGNLVMAVACMDROLKIKTNFYISLAFADLLVSLVMPF 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 STIRSVESCMFEGDFCLRLHTYLDLPTLSIFHLCTSIDRHCAI-CDPLLYPSKFT-V 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 GATLVODIWIYGEVFCVRSLSVLTLTASIFHLCCISIDRYAALICQPLVYRNKMTPL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 RVALRYILIAG-WGVPAAVTSFL-----YTDVETR-LSQWLEMPCYGSCOLLNKL 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 RIAL--MGGCQWVLPFTISFLPIMGWNNIGIILIERKNQNSSTYCV----FWYVK 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 FWG-WLNEPFLFVPCLLIMISLYKIEFVATROAOITTLSSLAGAKHER----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 PYATCSVAAYIFPLMLVLAIRIYVAKHAHQIQMLQR--AGASESPQSDQHS 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -----KAATLGIIVGIIYLLCWLPTIDTMVDSLHFTTPPLVDFITFAVNSACN 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 HRMRTETAAKTLCTIIMCCFCLCWAPEFVNTIVDPFDITVPGQWTAFLMLGYINSGLN 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 PIIVFSYQWFRKALKLTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 PFLYAFLNKSFRRAPLITL 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
PCT-US93-12586-8
; Sequence 8, Application PC/TUS9312586
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
```

REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93-12586-8

Query Match 25.5%; Score 455.5; DB 5; Length 388;
 Best local Similarity 34.5%; Pred. No. 4.7e-31;

Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVILYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLALADMFGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLIVAVVAVCDROLRIKTNCFIVSLAFADLVSVLMP 76
 QY 91 STIRVSCWCFEDFCLRLHTYDITLFCISIFHCISIDRCAI-CDPLYPSTFT-V 148
 DB 77 GALELVODIMWYGEVCLVTSIDVLTASIFHCISIDRYALCCOPLVYRNKMTPL 136
 QY 149 RVALRYTLAG-WGVPAAYTSFLF-----YTDVETR-LSQMLEMPCVSCOLLNK 198
 DB 137 RLNL-MLGSCWVYIPFISFLPMQGMNNGIIDLLEKRFNONSSTYCV---FMVKN 190
 QY 199 FNG-WLNFPLFVPCCLIMISLYKIFVATROAQITTLSSLAGAKHER----- 248
 DB 191 PVAITCSVAVFYIPFLMVLAVYRIYVTAKEHAHQIOMQR--AGASSESRPSADQHS 248
 QY 249 -----KAKTLGIYVGIYLCWLPFTIDTMDSLHFTTPPLVDFIWFAYFNSACN 301
 DB 249 HNRRTETKAKTKTICIMGCFCICMAFPFTVINVDPIDYTPQVWTAFLMGLYINSGLN 308
 QY 302 PIIVFSYQWFRKALRTL 320
 DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 10
 US-09-555-313B-2
 ; Sequence 2, Application US/09555313B
 ; Patent No. 6506580
 ; GENERAL INFORMATION:
 ; APPLICANT: FICSHMEISTER, Rudolph et al.
 ; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
 ; FILE REFERENCE: P067620500/BAS
 ; CURRENT APPLICATION NUMBER: US/09/555,313B
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: FR 97/15037
 ; PRIOR FILING DATE: 1997-11-28
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 760
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-555-313B-2

Query Match 25.5%; Score 455.5; DB 4; Length 760;
 Best local Similarity 34.5%; Pred. No. 9.6e-31;

Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVILYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLALADMFGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLIVAVVAVCDROLRIKTNCFIVSLAFADLVSVLMP 76
 QY 91 STIRVSCWCFEDFCLRLHTYDITLFCISIFHCISIDRCAI-CDPLYPSTFT-V 148

DB 77 GALELVODIMWYGEVCLVTSIDVLTASIFHCISIDRYAICCOPLVYRNKMTPL 136
 QY 149 RVALRYTLAG-WGVPAAYTSFLF-----YTDVETR-LSQMLEMPCVSCOLLNK 198
 DB 137 RLNL-MLGSCWVYIPFISFLPMQGMNNGIIDLLEKRFNONSSTYCV---FMVKN 190
 QY 199 FNG-WLNFPLFVPCCLIMISLYKIFVATROAQITTLSSLAGAKHER----- 248
 DB 191 PVAITCSVAVFYIPFLMVLAVYRIYVTAKEHAHQIOMQR--AGASSESRPSADQHS 248
 QY 249 -----KAKTLGIYVGIYLCWLPFTIDTMDSLHFTTPPLVDFIWFAYFNSACN 301
 DB 249 HNRRTETKAKTKTICIMGCFCICMAFPFTVINVDPIDYTPQVWTAFLMGLYINSGLN 308
 QY 302 PIIVFSYQWFRKALRTL 320
 DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 11
 US-07-996-772A-2
 ; Sequence 2, Application US/07996772A
 ; Patent No. 5472866
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe
 ; APPLICANT: Hartig, Paul R.
 ; APPLICANT: Branchek, Theresa A.
 ; APPLICANT: Weinshank, Richard L.
 ; TITLE OF INVENTION: DNA ENCODING 5-HT1A SEROTONIN
 ; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 ROCKEFELLER PLAZA
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/996,772A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, P., John
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 664-0525
 ; TELEFAX: 422523 COOP UI
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-996-772A-2

Query Match 25.0%; Score 446.5; DB 1; Length 387;
 Best local Similarity 33.1%; Pred. No. 2.7e-30;

Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

QY 33 IQLVILYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLALADMFGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLIVAVVAVCDROLRIKTNCFIVSLAFADLVSVLMP 76
 QY 91 STIRVSCWCFEDFCLRLHTYDITLFCISIFHCISIDRCAI-CDPLYPSTFT-V 148
 DB 77 GALELVODIMWYGEVCLVTSIDVLTASIFHCISIDRYAICCOPLVYRNKMTPL 136


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; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12586-2

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Query Match 25.0%; Score 446.5; DB 5; Length 387;
 Best Local Similarity 33.1%; Pred. No. 2.7e-30;
 Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

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QY 33 IOAVIYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPTNFTLLSLALADMFGLVLP 90
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 17 VERVVLLTFPAMVILMAIIGNLVMAVAVCDROLRIKIKYFTVSLAFADLVSVLVNAF 76
QY 91 STIRSVESCFPGDFLCRLHTYLDLFCLSIFHLCSIDRCAI-CDBLYPSKFT-V 148
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 77 GATELVQDIWFYEMCLVNTSIDVLLTTSIFHLCSIDRYALCCOGLVYRNKMTPL 136
QY 149 RVALRYILAG-WGVPAAYTSLF-----YTDVETR-----LSQMLEMPCVG 190
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 137 RIAL-MLGCCWVIPMFISFLPIMGWNNIGIVDIEKRKFNNNSSTFCVFNKPYAI 194
QY 191 SCOLLNKFEGWLNFLFEPCLIMISLYKIFVAVATRONQITTLKSLAGAAKHER-- 248
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 195 TCSVV-----AFYIPFLMLAVYRITYTAKENAOIOMLOR--AGATSESRPQ 241
QY 249 -----KAATLGIVGIIYLLCWLPTFTIDTVDSLLHFTTPPLVDFPIWFA 294
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 242 TADQSTHMRRTETKAKATLCVIMGCFCFMAFFVTNIVDPIDTVPEKVTATFLMG 301
QY 295 YFNSACNPIIYVFSYQMFRRALKLTL 320
Db 302 YINSGINPFLYAFNLKSFRRALFILL 327

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RESULT 15
 US-09-328-314-4
 ; Sequence 4, Application US/09328314
 ; Patent No. 6331401
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe
 ; APPLICANT: Hartig, Paul R.
 ; APPLICANT: Branchek, Theresa
 ; APPLICANT: Weinsbank, Richard L.

```

; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/328,314
; CURRENT FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 08/446,822
; EARLIER FILING DATE: 1995-07-31
; EARLIER APPLICATION NUMBER: PCT/US93/12586
; EARLIER FILING DATE: 1993-12-22
; EARLIER APPLICATION NUMBER: 07/996,772
; EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-328-314-4

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Query Match 25.0%; Score 446.5; DB 4; Length 406;
 Best Local Similarity 33.1%; Pred. No. 2.9e-30;
 Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

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QY 33 IOAVIYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPTNFTLLSLALADMFGLVLP 90
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 17 VERVVLLTFPAMVILMAIIGNLVMAVAVCDROLRIKIKYFTVSLAFADLVSVLVNAF 76
QY 91 STIRSVESCFPGDFLCRLHTYLDLFCLSIFHLCSIDRCAI-CDBLYPSKFT-V 148
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 77 GATELVQDIWFYEMCLVNTSIDVLLTTSIFHLCSIDRYALCCOGLVYRNKMTPL 136
QY 149 RVALRYILAG-WGVPAAYTSLF-----YTDVETR-----LSQMLEMPCVG 190
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 137 RIAL-MLGCCWVIPMFISFLPIMGWNNIGIVDIEKRKFNNNSSTFCVFNKPYAI 194
QY 191 SCOLLNKFEGWLNFLFEPCLIMISLYKIFVAVATRONQITTLKSLAGAAKHER-- 248
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 195 TCSVV-----AFYIPFLMLAVYRITYTAKENAOIOMLOR--AGATSESRPQ 241
QY 249 -----KAATLGIVGIIYLLCWLPTFTIDTVDSLLHFTTPPLVDFPIWFA 294
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 242 TADQSTHMRRTETKAKATLCVIMGCFCFMAFFVTNIVDPIDTVPEKVTATFLMG 301
QY 295 YFNSACNPIIYVFSYQMFRRALKLTL 320
Db 302 YINSGINPFLYAFNLKSFRRALFILL 327

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 Job time : 22 secs

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